

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 13, 2003, 07:52:21 / Search time 28 Seconds  
(without alignments)  
166.221 Million cell updates/sec

Title: US-09-759-112A-24  
Perfect score: 582  
Sequence: 1 DIVLTNSPALSIVSLGGRAT.....COLCNDPPPTFGAGTKLEIK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 328717  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537.5	92.4	132	2	US-08-483-636-2
2	537.5	92.4	132	2	US-08-483-632-2
3	519.5	89.3	111	1	US-08-491-845-8
4	516.5	88.7	131	3	US-08-579-378A-14
5	503.5	86.5	106	3	US-08-466-151-6
6	503.5	86.5	106	4	US-08-466-163B-6
7	491.5	84.5	111	3	US-08-466-151-2
8	491.5	84.5	111	4	US-08-466-163B-2
9	490.5	84.3	120	1	US-08-111-080-24
10	490.5	84.3	120	1	US-08-211-980-24
11	485.5	83.4	111	5	PCT-US93-07967-24
12	485.5	83.4	111	2	US-08-887-352B-5
13	485.5	83.4	111	2	US-09-109-207C-5
14	485.5	83.4	111	3	US-09-296-005-5
15	469.5	80.7	131	2	US-08-483-636-58
16	469.5	80.7	131	2	US-08-483-632-58
17	465.5	80.0	131	1	US-08-137-117D-33
18	465.5	80.0	131	2	US-08-436-717-33
19	463.5	79.6	131	2	US-08-483-636-14
20	463.5	79.6	131	2	US-08-483-632-14
21	460.5	79.1	131	2	US-08-137-117D-25
22	460.5	79.1	131	2	US-08-436-717-25
23	456.5	78.4	131	2	US-08-621-751A-10
24	453.5	77.9	111	1	US-08-275-053-11
25	453.5	77.9	121	1	US-08-111-080-22
26	453.5	77.9	121	1	US-08-211-980-22
27	453.5	77.9	121	5	PCT-US93-07967-22

28	449.5	77.2	111	2	US-08-483-636-73	Sequence 73, Appl
29	449.5	77.2	111	2	US-08-483-632-73	Sequence 73, Appl
30	448.5	77.1	129	4	US-09-556-605-2	Sequence 2, Appl1
31	447	76.8	151	4	US-09-318-786-33	Sequence 33, Appl
32	446.5	76.7	120	1	US-08-111-080-26	Sequence 26, Appl
33	446.5	76.7	120	1	US-08-211-980-26	Sequence 26, Appl
34	446.5	76.7	120	5	PCT-US93-07967-26	Sequence 26, Appl
35	444.5	76.4	111	1	US-08-207-169A-4	Sequence 4, Appl1
36	444.5	76.4	121	1	US-08-111-080-18	Sequence 18, Appl
37	444.5	76.4	121	1	US-08-211-980-18	Sequence 18, Appl
38	444.5	76.4	121	5	PCT-US92-07111-17	Sequence 17, Appl
39	444.5	76.4	121	5	PCT-US93-07967-18	Sequence 18, Appl
40	444	76.3	110	1	US-08-017-570-2	Sequence 2, Appl1
41	444	76.3	110	4	US-08-471-426-2	Sequence 2, Appl1
42	444	76.3	110	4	US-09-672-609-13	Sequence 13, Appl
43	444	76.3	110	4	US-09-025-403A-13	Sequence 13, Appl
44	444	76.3	110	5	PCT-US94-01709-2	Sequence 2, Appl1
45	439.5	75.5	132	2	US-08-379-057-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-08-483-636-2  
Sequence 2, Application US/08483636  
Patent No. 5914110  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corp./Corporate  
ADDRESS: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-483-636-2

Query Match 92.4%; Score 537.5; DB 2; Length 132;  
Best Local Similarity 93.7%; Pred. No. 2, 2e-49;  
Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRTATISCKASQSVYDGDSTW-WYQKPGQPKLLTYAASNLES 59  
DB 21 DIVLTQSPASLAVSLGQRTATISCKASQSVYDGDSTWMMYQKPGQPKLLTYAASNLES 80  
QY 60 GIPARFSGSGSTDFLTNIHPVEEDATYTCQNSNEDPPTGGTKLEIK 110  
DB 81 GIPARFSGSGSTDFLTNIHPVEEDATYTCQNSNEDPPTGGTKLEIK 131

## RESULT 2

US-08-483-632-2  
Sequence 2, Application US/08483632  
Patent No. 5928904

## GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TREATMENT OF IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UM2220  
CITY: King of Prussia  
STATE: PA

COUNTRY: USA  
ZIP: 19406-0939

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632

FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-632-2

Query Match 92.4%; Score 537.5; DB 2; Length 132;

Best Local Similarity 93.7%; Pred. No. 2, 2e-49;

Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRTATISCKASQSVYDGDSTW-WYQKPGQPKLLTYAASNLES 59  
DB 21 DIVLTQSPASLAVSLGQRTATISCKASQSVYDGDSTWMMYQKPGQPKLLTYAASNLES 80

DB 21 DIVLTQSPASLAVSLGQRTATISCKASQSVYDGDSTWMMYQKPGQPKLLTYAASNLES 80

QY 60 GIPARFSGSGSTDFLTNIHPVEEDATYTCQNSNEDPPTGGTKLEIK 110

DB 81 GIPARFSGSGSTDFLTNIHPVEEDATYTCQNSNEDPPTGGTKLEIK 131

## RESULT 3

US-08-491-845-8  
Sequence 8, Application US/08491845  
Patent No. 5773247

## GENERAL INFORMATION:

APPLICANT: MAEDA, Hiroaki  
APPLICANT: KIMACHI, Kazuhiko  
APPLICANT: EDA, Yasuyuki  
APPLICANT: SHIOSAKI, Kouichi  
APPLICANT: OSATOMI, Kiyoshi  
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
PROCESS FOR PREPARING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Browdy and Nelmark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,845

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00039

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: MAEDA-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-491-845-8

Query Match 89.3%; Score 519.5; DB 1; Length 111;

Best Local Similarity 91.9%; Pred. No. 1, 4e-47;

Matches 102; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRTATISCKASQSVYDGDSTW-WYQKPGQPKLLTYAASNLES 59  
DB 1 DIVLTQSPASLAVSLGQRTATISCKASQSVYDGDSTWMMYQKPGQPKLLTYAASNLES 60  
QY 60 GIPARFSGSGSTDFLTNIHPVEEDATYTCQNSNEDPPTGGTKLEIK 110  
DB 61 GIPARFSGSGSTDFLTNIHPVEEDATYTCQNSNEDPPTGGTKLEIK 111

## RESULT 4

US-08-579-378A-14  
Sequence 14, Application US/08579378A  
Patent No. 6210671

## GENERAL INFORMATION:

```

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-6

Query Match 86.5% Score 503.5; DB 3: Length 106;
Best Local Similarity 93.4%; Pred. No. 6,4e-46;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1

QY 1 DIVLTNSPASLAVSLGQRATISCKRASQSVVDYDGDSTM-WYQKPGQPPRLTLTYAASNTES 59
  |||
  1 DIQLTQSPASLAVSLGQRATISCKRASQSVVDYDGDSTMWYQKPGQPPRLTLTYAASNTES 60

QY 60 GIPARFSGSGSGCTDFTLNHPHVEEDATYYTCQLCNEPPFFGAGT 105
  |||
  61 GIPARFSGSGSGCTDFTLNHPHVEEDATYYTCQGSNEDPFTFGAGT 106

RESULT 6
: Sequence 6, Application US/08466163B
: Patent No. 6329509
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Priesta, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: FILE REFERENCE: P0718P2C1D1
: CURRENT APPLICATION NUMBER: US/08/466,163B
: CURRENT FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: US 08/405,617
: PRIOR FILING DATE: 1995-03-15
: PRIOR APPLICATION NUMBER: US 08/185,899
: PRIOR FILING DATE: 1994-01-26
: PRIOR APPLICATION NUMBER: US 07/879,495
: PRIOR FILING DATE: 1992-05-07
: PRIOR APPLICATION NUMBER: US 07/744,768
: PRIOR FILING DATE: 1991-08-14
: NUMBER OF SEQ ID NOS: 64

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SEQ ID NO 6  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Mus musculus  
US-08-466-163B-6

Query Match 86.5%; Score 503.5; DB 4; Length 106;  
Best Local Similarity 93.4%; Pred. No. 6.4e-46;  
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSICGCRATISCKASOSVDYDGSYM-WYQOKPQPKLLTYASNL5 59  
DB 1 DIVLTQSPASLAVSLGCRATISCKASOSVDYDGSYMWYQOKPQPKLLTYASNL5 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEDATYTCOLCNEDEPPTFGAGT 105  
DB 61 GIPARFSGSGGTDFTLNHPVEEDATYTCQOSHEDPTFGAGT 106

ULT 7  
DB-466-151-2  
Sequence 2, Application US/08466151  
Patent No. 6037453

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpulin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466.151  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-2

Query Match 84.5%; Score 491.5; DB 3; Length 111;

Best Local Similarity 88.3%; Pred. No. 1.2e-44;  
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSICGCRATISCKASOSVDYDGSYM-WYQOKPQPKLLTYASNL5 59  
DB 1 DIVLTQSPASLAVSLGCRATISCKASOSVDYDGSYMWYQOKPQPKLLTYASNL5 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEDATYTCOLCNEDEPPTFGAGTLEIK 110  
DB 61 EIPARFSGSGGTDFTLNHPVEEDATYTCQOSHEDPTFGAGTLEIK 111

RESULT 8  
US-08-466-163B-2

Sequence 2, Application US/08466163B  
Patent No. 6329509

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466.163B  
CURRENT FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07

PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64

SEQ ID NO 2  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Mus musculus  
US-08-466-163B-2

Query Match 84.5%; Score 491.5; DB 4; Length 111;  
Best Local Similarity 88.3%; Pred. No. 1.2e-44;  
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSICGCRATISCKASOSVDYDGSYM-WYQOKPQPKLLTYASNL5 59  
DB 1 DIVLTQSPASLAVSLGCRATISCKASOSVDYDGSYMWYQOKPQPKLLTYASNL5 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEDATYTCOLCNEDEPPTFGAGTLEIK 110  
DB 61 EIPARFSGSGGTDFTLNHPVEEDATYTCQOSHEDPTFGAGTLEIK 111

RESULT 9  
US-08-111-080-24

Sequence 24, Application 08/111080  
Patent No. 555865

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:



APPLICATION NUMBER: 08/111,080  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-111-080-24

Query Match 84.3%; Score 490.5; DB 1; Length 120;  
Best Local Similarity 87.3%; Pred. No. 1.7e-44;  
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASIYSLGGRATISCKASOSVDYDGSYM-WYQKRGOPPKLITYASNL5 59  
Db 1 DIVLTQSPASIASVSLGGRATISCKASOSVDYDGSYMMWYQKRGOPPKLITYASNVES 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQLCNEDPPTFGAGTKLEL 109  
Db 61 GIPARFYGSGGTDFTLNHPVEEEDATYYCQCSIDDPSIFGSGTKLEI 110

RESULT 10  
US-08-211-980-24  
Sequence 24, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-24

Query Match 84.3%; Score 490.5; DB 1; Length 120;  
Best Local Similarity 87.3%; Pred. No. 1.7e-44;  
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASIYSLGGRATISCKASOSVDYDGSYM-WYQKRGOPPKLITYASNL5 59  
Db 1 DIVLTQSPASIASVSLGGRATISCKASOSVDYDGSYMMWYQKRGOPPKLITYASNVES 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQLCNEDPPTFGAGTKLEL 109  
Db 61 GIPARFYGSGGTDFTLNHPVEEEDATYYCQCSIDDPSIFGSGTKLEI 110

RESULT 11  
PCT-US93-07967-24  
Sequence 24, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-07967-24



STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25Z  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
OS-08-483-636-58

Query Match	80.7%	Score 469.5;	DB 2;	Length 131;
Best Local Similarity	80.2%	Pred. No. 3.1e-42;		
Matches	89;	Conservative	8;	Mismatches 13;
			Indels	1;
			Gaps	1;

[illegible]

Search completed: September 13, 2003, 07:56:02  
Job time : 30 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 06:42:50 : Search time 74 Seconds  
(without alignments)  
235.945 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582

Sequence: 1 DIVLTPNSPLAVSLGGRAT.....COLCNDPPPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_19Jun03.\*

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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
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- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	100.0	110	23	AAO18536
2	537.5	92.4	132	16	AAO18536
3	537.5	92.4	132	20	AAO18536
4	537.5	92.4	132	20	AAO18536
5	532.5	91.5	111	21	AAO18536
6	532.5	91.5	111	21	AAO18536
7	532.5	91.5	111	21	AAO18536
8	532.5	91.5	111	21	AAO18536
9	532.5	91.5	111	21	AAO18536

10	532.5	91.5	305	21	AAO18536
11	532.5	91.5	305	21	AAO18536
12	528.5	90.8	238	19	AAO18536
13	528.5	90.8	238	21	AAO18536
14	528.5	90.8	238	21	AAO18536
15	528.5	90.8	238	21	AAO18536
16	528.5	90.8	238	21	AAO18536
17	526.5	90.5	238	23	AAO18536
18	526.5	90.5	238	24	AAO18536
19	522.5	89.8	111	15	AAO18536
20	522.5	89.8	111	15	AAO18536
21	521.5	89.6	131	14	AAO18536
22	519.5	89.3	111	10	AAO18536
23	519.5	89.3	111	10	AAO18536
24	519.5	89.3	111	10	AAO18536
25	515.5	88.6	113	22	AAO18536
26	512.5	88.1	122	18	AAO18536
27	511.5	87.9	131	11	AAO18536
28	503.5	86.5	106	14	AAO18536
29	503.5	86.5	106	21	AAO18536
30	503.5	86.5	112	22	AAO18536
31	498.5	85.7	103	21	AAO18536
32	498.5	85.7	103	21	AAO18536
33	491.5	84.5	111	14	AAO18536
34	491.5	84.5	111	21	AAO18536
35	490.5	84.3	120	15	AAO18536
36	487.5	83.8	218	15	AAO18536
37	487.5	83.8	218	24	AAO18536
38	487.5	83.8	238	19	AAO18536
39	487.5	83.8	238	21	AAO18536
40	487.5	83.8	238	21	AAO18536
41	487.5	83.8	238	23	AAO18536
42	487.5	83.8	238	23	AAO18536
43	485.5	83.4	111	20	AAO18536
44	485.5	83.4	111	20	AAO18536
45	476.5	81.9	238	19	AAO18536

#### ALIGNMENTS

RESULT 1	AAO18536
ID	AAO18536 standard; Protein; 110 AA.
XX	AAO18536;
XX	11-OCT-2002 (first entry)
DE	Murine Mab 1F7 light chain.
XX	
KW	Mouse: 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
KW	complementarity determining region; framework-determining region;
KW	FR; heavy chain; light chain; HIV infection.
XX	
OS	Mus sp.
XX	
PN	W0200255668-A2.
PD	18-JUL-2002.
XX	
PE	11-JAN-2002; 2002MO-US00927.
XX	
PR	11-JAN-2001; 2001US-0759112.
XX	
PA	(IMMP- ) IMMOPHERON INC.
XX	
PI	Muller S. Kohler H;
XX	
DR	WPI; 2002-590668/63.
DR	N-PSDB; AAL48661.
XX	
PT	New polynucleotide encoding a complementarity- or framework-determining

Murine derived pro  
Murine derived pro  
Anti-Fas Mab HFF7A  
Mouse anti-Fas ant  
Murine anti-Fas an  
Humanised anti-Fas  
Humanised anti-Fas  
Human penton base  
Mouse DAV-1 light  
Mouse anti-HIV mAb  
Anti HIV antibody  
Immunoglobulin L c  
Mouse AC10 antibody  
Amino acids sequen  
Monoclonal antibod  
MHI monoclonal ant  
Anti-Lau 3a light  
Maetis light chain.  
Light chain amino  
Anti-SAF-1 monoclo  
Antibody 4H5 L cha  
Murine derived pro  
Maetis light chain.  
Light chain amino  
Sequence of the mo  
TSH receptor antib  
Anti-Fas humanised  
Humanised anti-Fas  
Humanised anti-Fas  
Humanised anti-Fas  
Humanised anti-Fas  
Mus musculus anti-  
Variable light cha  
Anti-Fas humanised





```

AC AAVS1144;
XX
XX 31-MAR-2000 (first entry)
DT
DE Murine derived protein fragment #6.
XX
XX Cluster differentiation: cell separation; antibody: CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KM HIV infection; autoimmune disease; murine.
XX
OS Mus sp.
XX
XX MO9961629-A1.
XX
XX 02-DEC-1999.
XX
XX PD
XX PE 24-MAY-1999; 99WO-JP02711.
XX
XX PR 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX
XX (ASAH ) ASAMI KASEI KOGYO KK.
XX (ASAH ) ASAHI MEDICAL CO LTD.
XX
XX Ono M, Soka T, Morimoto I, Miyamura K;
PI WPI: 2000-086720/07.
XX
XX Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells -
XX
XX Disclosure: Page 95; 111pp: Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for
CC the collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal
CC compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX
XX Sequence 111 AA:
SO
Query Match 91.5%; Score 532.5; DB 21; Length 111;
Best Local Similarity 92.8%; Pred. No. 2,3e-38;
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1
DB 1 DIVLTNSPASISLAVSLGOKRATISKCKSSQSYVDYDGSYM-WYOOKPGOPPKLLTYAASNLES 59
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 1 DIVLTQSAPASIAVSLGOKRATISKCKSSQSYVDYDGSYMNWYOOKPGOPPKLLTYAASNLES 60
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
QY 60 GIPAFSSGSGCTDFTLNINHPVEEDDAATYYCOLCNEBDDPPRTGAGKLEIK 110
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 61 GIPAFSSGSGCTDFTLNINHPVEEDDAATYYCOQSSSEDPRTGGGKLEIK 111
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

RESULT 7
AAVS1146
ID AAVS1146 standard; Protein: 111 AA.
XX
XX AAVS1146;
XX
XX 31-MAR-2000 (first entry)
XX
XX Murine derived protein fragment #8.
XX
XX Cluster differentiation: cell separation; antibody: CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KM HIV infection; autoimmune disease; murine.
XX

```

[illegible]





XX AAV51142;  
 AC 31-MAR-2000 (first entry)  
 XX Murine derived protein fragment #4.  
 DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KM HIV infection; autoimmune disease; murine.  
 XX Mus sp.  
 OS WO9961629-A1.  
 PM 02-DEC-1999.  
 PD 24-MAY-1999; 99WO-JP02711.  
 PF 25-MAY-1998; 98JP-0159957.  
 XX 26-MAY-1998; 98JP-0163023.  
 (ASAH ) ASAH KASEI KOCYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 DR WPI: 2000-086720/07.  
 DR N-PSDB; AA244206.  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells  
 PS Claim 22; Page 82-84; 11pp; Japanese.  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 SO Sequence 305 AA;  
 Query Match 91.5%; Score 532.5; DB 21; Length 305;  
 Last Local Similarity 92.8%; Pred. No. 6.3e-38;  
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASIYAVSGORATISCKASOSVDYDGSYM-WYQOKPGOPKLLTYASNLNS 59  
 DB 156 DIVLTQSPASIVASIGORATISCKASOSVDYDGSYMMWYQOKPGOPKLLTYASNLNS 215  
 QY 60 GIPARFSGSGGTDTFTLNHPVEEDATYTCQLCNEDPPTFGAGTKLEIK 110  
 DB 216 GIPARFSGSGGTDTFTLNHPVEEDATYTCQOSEDPPTFGAGTKLEIK 266  
 RESULT 12  
 AAW83042  
 ID AAW83042 standard; Protein; 238 AA.  
 XX AAW83042;  
 AC 25-MAR-2003 (updated)  
 DT 15-MAR-1999 (first entry)  
 XX Anti-Fas MAB HFE7A light chain.  
 DE HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KM systemic lupus erythematosus; graft versus host disease;  
 KM Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KM scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KM rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KM myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KM thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KM atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KM glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KM transplant rejection; therapy; complementarity determining region;  
 CDR.  
 XX Mus musculus.  
 OS  
 XX Key Location/Qualifiers  
 FH 1..20  
 FT Peptide /label= Sig\_peptide  
 FT 21..238  
 FT Protein /label= Mat\_protein  
 FT 21..131  
 FT Region /label= Variable  
 FT 132..238  
 FT Region /label= Constant  
 FT 44..58  
 FT Region /label= CDR\_L1  
 FT /note= "claim 9"  
 FT 74..80  
 FT Region /label= CDR\_L2  
 FT /note= "claim 9"  
 FT 113..121  
 FT Region /label= CDR\_L3  
 FT /note= "claim 9"  
 AU9859701-A.  
 08-OCT-1998.  
 30-MAR-1998; 98AU-0059701.  
 08-OCT-1997; 97JP-0276064.  
 01-APR-1997; 97JP-0082953.  
 25-JUN-1997; 97JP-0169088.  
 (SANY ) SANKYO CO LTD.  
 AKIO S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 Masahiko O, Nobufusa S, Shin Y, Rohru T;  
 WPI: 1998-543440/01.  
 DR N-PSDB; AAV70130.  
 DR New antibodies and proteins bind conserved epitope of Fas antigen -  
 DR used to evaluate drugs in animal models and to treat Fas-associated  
 DR diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 PT  
 XX Reference Example 4: Page 189-190; 292pp; English.  
 PS This is the amino acid of the light chain of murine anti-human Fas  
 CC monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light  
 CC chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)  
 CC RNA by RT-PCR (see AAV0127-28). The invention provides humanised  
 CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These  
 CC antibodies are capable of inducing apoptosis in abnormal cells  
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
 CC cells. They are used to evaluate, in animal models, treatments of  
 CC diseases that involve Fas/Fas ligand interactions, and also to treat  
 CC such diseases, including autoimmune disease (e.g. systemic lupus  
 CC erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,  
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:50:50 ; Search time 37 Seconds  
(Without alignments)  
285.907 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582

Sequence: 1 DIVLTNSPASPASLAVSLGQRAT.....COLCNEDEPPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR\_76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	91.7	111	1	KVMS83
2	527.5	90.6	111	1	KVMS43
3	523.5	89.9	111	1	KVMS08
4	521.5	89.6	112	2	S19971
5	521.5	89.6	131	2	PH1226
6	520.5	89.4	111	1	KVMS69
7	505	86.8	110	1	KVMS10
8	503.5	86.5	111	1	KVMS01
9	502.5	86.3	112	2	S19976
10	485.5	83.4	112	2	S19972
11	476.5	81.9	111	2	S09966
12	473.5	81.4	111	1	KVMS75
13	470.5	80.8	111	1	KVMS40
14	468.5	80.5	111	1	KVMS84
15	457.5	78.6	112	2	S45715
16	455.5	78.3	111	1	KVMS37
17	454.5	78.1	111	1	KVMS85
18	452.5	77.7	131	2	S55027
19	451.5	77.6	210	2	A56169
20	449.5	77.2	218	2	JCS810
21	448.5	77.1	131	1	KVMS06
22	445.5	76.5	218	2	S68241
23	442.5	76.0	115	2	S63596
24	441.5	75.9	93	2	A38601
25	438.5	75.3	111	2	S09963
26	438.5	75.3	111	2	D45722
27	432.5	74.3	111	1	KVMS80
28	430.5	74.0	107	2	S26343
29	430.5	74.0	107	2	S26344

30	430.5	74.0	108	1	KVMS54	Ig kappa chain V r
31	429.5	73.8	111	2	PL0081	Ig kappa chain V r
32	428.5	73.6	111	1	KVMS50	Ig kappa chain V r
33	428	73.5	110	2	S24288	Ig kappa chain V r
34	427.5	73.3	111	2	S09969	Ig kappa chain V-J
35	426.5	73.3	140	2	PN0446	Ig kappa chain pre
36	424.5	72.9	132	1	KVMS32	Ig kappa chain pre
37	421.5	72.4	111	2	S09965	Ig kappa chain V-J
38	417.5	71.7	102	2	PH1076	Ig light chain V r
39	417	71.6	108	2	PH0092	Ig kappa chain V r
40	415.5	71.4	109	2	PH0093	Ig kappa chain V r
41	415.5	71.4	111	2	E53285	Ig kappa chain V r
42	410	70.4	233	2	CJ5322	Ig kappa chain V a
43	405.5	69.7	102	2	PH1077	p53 specific singl
44	405.5	69.7	102	2	PH1079	Ig light chain V r
45	403.5	69.3	111	2	S37202	Ig light chain V r

#### ALIGNMENTS

RESULT 1  
KVMS83  
Ig kappa chain V region (PC7183) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: B01937; A01937  
R:Weigert, M.; Galtaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; M0ID:79073152; PMID:103003  
A:Accession: B01937  
A:Molecule type: protein  
A:Residues: 1-111 <MBL>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 91.7%; Score 533.5; DB 1; Length 111;  
Best Local Similarity 94.6%; Pred. No. 2.6e-41;  
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASQSDYDGDSTW-WYQKPGQPKLLTYAASNLES 59  
|||||  
Db 1 DIVLTNSPASPASLAVSLGQRATISCKASQSDYDGDSTWYQKPGQPKLLTYAASNLES 60  
QY 60 GIPARFSGSGGDTFLNTHPVEEDATYYCOQSNEDPPTFGAGTKLELK 110  
|||||  
Db 61 GIPARFSGSGGDTFLNTHPVEEDATYYCOQSNEDPPTFGAGTKLELK 111

RESULT 2  
KVMS43  
Ig kappa chain V region (PC7043) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
C:Accession: A01937; S42187; S42190; S42189; S42188; S42191; S42192  
R:Weigert, M.; Galtaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; M0ID:79073152; PMID:103003  
A:Accession: A01937  
A:Molecule type: protein  
A:Residues: 1-111 <MBL>  
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993  
A>Title: Variable region gene selection of immunoglobulin G-expressing B cells with s  
A:Reference number: S42176; M0ID:94009207; PMID:7691608  
A:Accession: S42187  
A:Molecule type: DNA

A:Residues: 10-99 <MO>  
 A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42194  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42190  
 A:Molecule type: DNA  
 A:Residues: 13-99 <MO>  
 A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42189  
 A:Molecule type: DNA  
 A:Residues: 15-99 <MO>  
 A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42188  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42191  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42192  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843  
 A:Note: V-kappa-21E; anti-collagen  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 90.6%; Score 527.5; DB 1; Length 111;  
 Best Local Similarity 92.8%; Pred. No. 8.9e-41;  
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Oy 1 DIVLTNSPASLAVSLGQRATISCKASQSVDDGDSY-WYQOKRGQPPKLTLYASNLES 59  
 |||||  
 Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVDDGDSYMWYQOKRGQPPKLTLYASNLES 60  
 60 GIPARFSGSGSGTDFTLNHPEVEDAATYYCQLCNEDPPTFGATLEIK 110  
 |||||  
 61 GIPARFSGSGSGTDFTLNHPEVEDAATYYCQSQSNEDPPTFGSGTLEIK 111

RESULT 3  
 KVM508  
 Ig kappa chain V region (PC6308) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: C01937; A01937  
 R:Weigert, M.; Gammelman, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Accession number: A93204; MUID:79073152; PMID:103003  
 A:Accession: C01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WT>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IM>  
 F:23-92/Disulfide bonds: #status predicted

```

Query Match 89.9%; Score 523.5; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 2e-40;
Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAIVSLGQRATISCKASQSVDDYDGSYM-WYQQRKGPCKLLTYAASNLES 59
    |||||
DB 1 DIVLTQSPASLAPMSLQGRATISCKASQSVDDYDGSYMNWYQQRKGPCKLLTYAASNLES 60
    |||||

60 GIPARFSGSGSGDTFTLNHPVEEEDATATYCCLNEDPPTFGAGTKLEIK 110
    |||||
61 GIPARFSGSGSGDTFTLNHPVEEEDATATYCCQNSNEDPPTFGSGTKLEIK 111
    |||||

RESULT 4
SI9971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9971; SI9973
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9971
A:Molecule type: mRNA
A:Residues: 1-112 <WEB>
A:Cross-references: EMBL:X65092; NID:g522288; PIDN:CAA6219.1; PID:g52289
A:Experimental source: clone M-T310
A:Accession: SI9973
A:Molecule type: mRNA
A:Residues: 1-112 <WEB>
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA6220.1; PID:g52293
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 89.6%; Score 521.5; DB 2; Length 112;
Best Local Similarity 90.1%; Pred. No. 3.1e-40;
Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAIVSLGQRATISCKASQSVDDYDGSYM-WYQQRKGPCKLLTYAASNLES 59
    |||||
DB 1 DIVLTQSPASLAPMSLQGRATISCKASQSVDDYDGSYMNWYQQRKGPCKLLTYAASNLES 60
    |||||

60 GIPARFSGSGSGDTFTLNHPVEEEDATATYCCLNEDPPTFGAGTKLEIK 110
    |||||
61 GIPARFSGSGSGDTFTLNHPVEEEDATATYCCQNSNEDPPTFGGKTKLEIK 111
    |||||

RESULT 5
PH1226
Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1226
R:Weissenhorn, W.; Scheuer, W.; Kaluzs, B.; Schirzke, M.; Reiter, C.; Flieger, D.; L
Gene 121, 271-276, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and
A:Reference number: PH1224; MUID:93077041; PMID:1446824
A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEB>
A:Cross-references: GB:SS0265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A:Note: This mouse sequence was hybridized and fused with a human constant region gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 89.6%; Score 521.5; DB 2; Length 131;
Best Local Similarity 90.1%; Pred. No. 3.6e-40;

```

Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGOPPKLLTYAASNLES 59

Db 21 DIVLTGSPASLAVSLGQRATISCKASOSLDYDSDSYNMYQKPGOPPKLLTYAASNLES 80

QY 60 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 81 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCQSSDEPTFGGKLEIK 131

#### RESULT 6

KVMS69

Ig kappa chain V region (PC7769) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000

C:Accession: E01937; A01937

R:Weigert, M.; Galtmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Title: Rearrangement of genetic information may produce immunoglobulin diversity.

Reference number: A93204; MUID:79073152; PMID:103003

Accession: E01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 89.4%; Score 520.5; DB 1; Length 111;

Best Local Similarity 91.0%; Pred. No. 3.8e-40;

Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSVDYDSDSYNMYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCQSSDEPTFGGKLEIK 111

#### RESULT 7

KVMS10

Ig kappa chain V region (PC7210) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000

C:Accession: D01937; A01937

R:Weigert, M.; Galtmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Title: Rearrangement of genetic information may produce immunoglobulin diversity.

Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: D01937

A:Molecule type: protein

A:Residues: 1-110 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 86.8%; Score 505; DB 1; Length 110;

Best Local Similarity 90.1%; Pred. No. 9.4e-39;

Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSLDYDSDSYNMYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCQ-SEDPPTFGGKLEIK 110

#### RESULT 8

KVMS1

Ig kappa chain V region (CAPC 101) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000

C:Accession: A01936

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related

A:Reference number: A93822; MUID:79012520; PMID:99744

A:Accession: A01936

A:Molecule type: protein

A:Residues: 1-111 <MKC>

C:Comment: This chain was isolated from a myeloma protein.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 86.5%; Score 503.5; DB 1; Length 111;

Best Local Similarity 89.2%; Pred. No. 1.3e-38;

Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSVDYDSDSYNMYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCQSSDEPTFGGKLEIK 111

#### RESULT 9

S19976

Ig kappa chain V region (M-T413) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S19976

R:Weissenborn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19976

A:Molecule type: preliminary

A:Residues: 1-112 <WEI>

C:Cross-references: EMBL:X65093; NID:952298; PIDN:CAA46221.1; PID:952299

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 502.5; DB 2; Length 112;

Best Local Similarity 88.3%; Pred. No. 1.6e-38;

Matches 98; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSLDYDSDSYNMYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGSGTDFLTNIHPVEEDAAATYCCQSSIDDPYTFGGGKLEIK 111

#### RESULT 10

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:45:09 ; Search time 23 Seconds  
(without alignments)  
224.910 Million cell updates/sec

Title: US-09-759-112a-24

Sequence: 1 DIVLTNSPASTAVSLGQRAT.....COLCNEPPTFGAGTKLEIK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533.5	91.7	111	1	KV3N_MOUSE
2	527.5	90.6	111	1	KV3M_MOUSE
3	523.5	89.9	111	1	KV3O_MOUSE
4	520.5	89.4	111	1	KV3O_MOUSE
5	505	86.8	110	1	KV3P_MOUSE
6	503.5	86.5	111	1	KV3L_MOUSE
7	473.5	81.4	111	1	KV3S_MOUSE
8	470.5	80.8	111	1	KV3R_MOUSE
9	468.5	80.5	111	1	KV3R_MOUSE
10	455.5	78.3	111	1	KV3H_MOUSE
11	455.5	78.3	111	1	KV3K_MOUSE
12	454.5	78.1	111	1	KV3U_MOUSE
13	449.5	77.2	111	1	KV3J_MOUSE
14	448.5	77.1	111	1	KV3I_MOUSE
15	435.5	74.8	111	1	KV3C_MOUSE
16	433	74.4	112	1	KV3B_MOUSE
17	432.5	74.3	111	1	KV3A_MOUSE
18	430.5	74.0	108	1	KV3V_MOUSE
19	428.5	73.6	111	1	KV3D_MOUSE
20	424.5	72.9	112	1	KV3G_MOUSE
21	424.5	72.9	112	1	KV3F_MOUSE
22	392.5	67.4	111	1	KV3E_MOUSE
23	373.5	64.2	114	1	KV4A_MOUSE
24	371.5	63.8	134	1	KV4C_MOUSE
25	366	62.9	133	1	KV4B_MOUSE
26	352.5	60.6	108	1	KV5P_MOUSE
27	351	60.3	129	1	KV3H_HUMAN
28	350.5	60.2	108	1	KV1M_HUMAN
29	344	59.1	109	1	KV3D_HUMAN
30	343	58.9	129	1	KV3L_HUMAN
31	340	58.4	109	1	KV3F_HUMAN
32	339	58.2	109	1	KV3B_HUMAN
33	337.5	58.0	108	1	KV1K_HUMAN

34	337.5	58.0	129	1	KV1M_HUMAN	P04431	homo sapien
35	336	57.7	129	1	KV3M_HUMAN	P18136	homo sapien
36	335.5	57.6	108	1	KV1H_HUMAN	P01600	homo sapien
37	333.5	57.3	108	1	KV1N_HUMAN	P01606	homo sapien
38	333	57.2	113	1	KV2G_MOUSE	P01631	mus musculus
39	331.5	57.0	108	1	KV1F_HUMAN	P01538	homo sapien
40	331.5	57.0	108	1	KV1G_HUMAN	P01539	homo sapien
41	329.5	56.6	121	1	KV4O_HUMAN	P06312	homo sapien
42	328.5	56.4	108	1	KV1B_HUMAN	P01594	homo sapien
43	328	56.4	133	1	KV2E_HUMAN	P06310	homo sapien
44	327.5	56.3	108	1	KV1E_HUMAN	P01537	homo sapien
45	327	56.2	109	1	KV3E_HUMAN	P01623	homo sapien

## ALIGNMENTS

RESULT 1	ID	KV3N_MOUSE	STANDARD:	PRT:	111 AA.
AC	P01666:	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, last annotation update)				
DE	Ig kappa chain V-II region PC 7183.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=79073152; PubMed=103003;				
RA	Wiegert M, Gattaman L, Loh E, Schilling J, Hood L.E.				
RT	"Rearrangement of genetic information may produce immunoglobulin diversity."				
RL	Nature 276:785-790(1978).				
DR	PIR; B01937; KWS83.				
DR	HSSP; P01679; 2FBJ.				
DR	InterPro: IPR007110; Ig-like.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IgV_1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 38				
FT	DOMAIN 39 53				
FT	DOMAIN 54 60				
FT	DOMAIN 61 92				
FT	DOMAIN 93 101				
FT	DOMAIN 102 111				
FT	DISULFID 23 92				
FT	NON_TER 111 111				
SO	SEQUENCE 111 AA; 11952 MW; 2058BB50CE306031 CRC64;				
Query Match	91.7%; Score 533.5; DB 1; Length 111;				
Best Local Similarity	94.6%; Pred. No. 1.8e-46;				
Matches 105; Conservative	0; Mismatches 5; Indels 1; Gaps 1;				
OY	1 DIVLTNSPASTAVSLGQRATISCKASQSVYDGDSTYMWYQOKPGOPPKLITYAASNLDS 59				
DB	1 DIVLTNSPASTAVSLGQRATISCKASQSVYDGDSTYMWYQOKPGOPPKLITYAASNLDS 60				
OY	60 GIDARPSGSGSDFTLNHPVEEDATATYCOLCNEPPTFGAGTKLEIK 110				
DB	61 GIDARPSGSGSDFTLNHPVEEDATATYCOLCNEPPTFGAGTKLEIK 111				
RESULT 2					
KV3M_MOUSE	STANDARD;				
ID	KV3M_MOUSE				
AC	P01665;				

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DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7043.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL diversity.";
RL Nature 276:785-790(1978).
DR HSSP: P80362; KWMS43.
DR InterPro: IPR003006; Ig_1like.
DR InterPro: IPR003596; Ig_V.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 93 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 102 111 FRAMEWORK-4.
FT NON_TER 23 92 BY SIMILARITY.
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 90.6%; Score 527.5; DB 1; Length 111;
Best Local Similarity 92.8%; Pred. No. 7,2e-46;
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

OY 1 DIVLTNSPASLAVSIGORATISCKASQSVYDGDSDYM-WYQOKPGOPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSIGORATISCKASQSVYDGDSDYMMWYQOKPGOPKLLTYAASNLES 60
OY 60 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQLCNEDPPFTGAGTKLEIK 110
DB 61 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQSNEDPPFTGSGTKLEIK 111

MULT 3
O_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 6308.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL diversity.";
RL Nature 276:785-790(1978).
DR HSSP: P80362; KWMS08.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00047; Ig; 1.

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DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 93 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 102 111 FRAMEWORK-4.
FT NON_TER 23 92 BY SIMILARITY.
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 89.9%; Score 523.5; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 1.8e-45;
Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIVLTNSPASLAVSIGORATISCKASQSVYDGDSDYM-WYQOKPGOPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSIGORATISCKASQSVYDGDSDYMMWYQOKPGOPKLLTYAASNLES 60
OY 60 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQLCNEDPPFTGAGTKLEIK 110
DB 61 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQSNEDPPFTGSGTKLEIK 111

RESULT 4
KV3Q_MOUSE STANDARD; PRT; 111 AA.
ID KV3Q_MOUSE
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7769.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL diversity.";
RL Nature 276:785-790(1978).
DR HSSP: P80362; KWMS69.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 93 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 102 111 FRAMEWORK-4.
FT NON_TER 23 92 BY SIMILARITY.
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 89.4%; Score 520.5; DB 1; Length 111;
Best Local Similarity 91.0%; Pred. No. 3.6e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

OY 1 DIVLTNSPASLAVSIGORATISCKASQSVYDGDSDYM-WYQOKPGOPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSIGORATISCKASQSVYDGDSDYMMWYQOKPGOPKLLTYAASNLES 60

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OY 60 GIPARFSGSGTDFLTINHPVEEDATATYCCOLCNEDEPTFGAGTKLEIK 110  
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGSGTKLEIK 111

## RESULT 5

KV3P\_MOUSE STANDARD; PRT; 110 AA.  
 ID KV3P\_MOUSE  
 AC P01668;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7210.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

## [1]

SEQUENCE.  
 MEDLINE=79073152; PubMed=103003;  
 Weigert M., Gattalitan L., Loh E., Schilling J., Hood L.E.;  
 "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 Nature 276:785-790(1978).  
 RT Nature 276:785-790(1978).  
 RL PIR: D01937; KWS10.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_V.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 101 110 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 110 110  
 SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE86B1249 CRC64;

Query Match 86.8%; Score 505; DB 1; Length 110;  
 Best Local Similarity 90.1%; Pred. No. 1.2e-43;  
 Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

DB 1 DIVLTNSPASTAVSLGCRATISCKASQSVYDGDSDVM-WYQKPGCPKLLTYAASLLES 59  
 1 DIVLTGSPASLAVSLGCRATISCKASQSLDYDGSINMWNWYQKPGCPKLLTYAASLLES 60  
 OY 60 GIPARFSGSGTDFLTINHPVEEDATATYCCOLCNEDEPTFGAGTKLEIK 110  
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGSGTKLEIK 110

## RESULT 6

KV3L\_MOUSE STANDARD; PRT; 111 AA.  
 ID KV3L\_MOUSE  
 AC P01664;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region CBPC 101.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 MEDLINE=79012520; PubMed=99744;

RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions";  
 RL Proc. Natl. Acad. Sci. U.S.A. 73:3913-3917(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MELOMA PROTEIN.

DR PIR: A01936; KWS1.  
 DR HSSP: P80362; 1WTL.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11964 MW; EZBIAD98AD965962 CRC64;

Query Match 86.5%; Score 503.5; DB 1; Length 111;  
 Best Local Similarity 89.2%; Pred. No. 1.8e-43;  
 Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTAVSLGCRATISCKASQSVYDGDSDVM-WYQKPGCPKLLTYAASLLES 59  
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGAGTKLEIK 111  
 OY 60 GIPARFSGSGTDFLTINHPVEEDATATYCCOLCNEDEPTFGAGTKLEIK 110  
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGAGTKLEIK 111

## RESULT 7

KV3S\_MOUSE STANDARD; PRT; 111 AA.  
 ID KV3S\_MOUSE  
 AC P01671;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7175.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gattalitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 Nature 276:785-790(1978).  
 RL Nature 276:785-790(1978).  
 DR PIR: B01938; KWS75.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.

FT DISULEID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 81.4%; Score 473.5; DB 1; Length 111;  
 Best Local Similarity 85.6%; Pred. No. 1.7e-40;  
 Matches 95; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

OY 1 DIVLTNSPASPASLAVSLGQARATISCKASQSYVDGDSYM-WYQKPGCPKLLTYAASNLDS 59  
 DB 1 DIVLTNSPASPASLAVSLGQARATISCKASQSYVDGDSYM-WYQKPGCPKLLTYAASNLDS 60  
 OY 60 GIPARFSGSGSGTDFLTNIHPVEEDDAATYYCOLCNEPPTGAGTKLELK 110  
 DB 61 GVPARFSGSGSGTDFLTNIHPVEEDDAATYYCOHSRELPLTFGAGTKLELK 111

RESULT 8  
 KV3T\_MOUSE STANDARD; PRT; 111 AA.

P01672;  
 21-JUL-1986 (rel. 01, Created)  
 21-JUL-1986 (rel. 01, Last sequence update)  
 15-JUL-1999 (rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7940.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: C01938; KYMS40.  
 DR HSSP: P80362; IWTL.  
 DR InterPro: IPR007110; Ig\_1like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 60 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULEID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12038 MW; EE8A82306084352E CRC64;

Query Match 80.8%; Score 470.5; DB 1; Length 111;  
 Best Local Similarity 83.8%; Pred. No. 3.4e-40;  
 Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

OY 1 DIVLTNSPASPASLAVSLGQARATISCKASQSYVDGDSYM-WYQKPGCPKLLTYAASNLDS 59  
 DB 1 DIVLTNSPASPASLAVSLGQARATISCKASQSYVDGDSYM-WYQKPGCPKLLTYAASNLDS 60  
 OY 60 GIPARFSGSGSGTDFLTNIHPVEEDDAATYYCOLCNEPPTGAGTKLELK 110  
 DB 61 GVPARFSGSGSGTDFLTNIHPVEEDDAATYYCOHSRELPLTFGAGTKLELK 111

RESULT 9  
 KV3R\_MOUSE STANDARD; PRT; 111 AA.  
 ID KV3R\_MOUSE  
 AC P01670;

DT 21-JUL-1986 (rel. 01, Created)  
 DT 21-JUL-1986 (rel. 01, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 6684.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: A01938; KYMS84.  
 DR HSSP: P80362; IWTL.  
 DR InterPro: IPR007110; Ig\_1like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 60 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULEID 23 92 FRAMEWORK-4.  
 FT NON\_TER 111 111 BY SIMILARITY.  
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 80.5%; Score 468.5; DB 1; Length 111;  
 Best Local Similarity 83.8%; Pred. No. 5.4e-40;  
 Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

OY 1 DIVLTNSPASPASLAVSLGQARATISCKASQSYVDGDSYM-WYQKPGCPKLLTYAASNLDS 59  
 DB 1 DIVLTNSPASPASLAVSLGQARATISCKASQSYVDGDSYM-WYQKPGCPKLLTYAASNLDS 60  
 OY 60 GIPARFSGSGSGTDFLTNIHPVEEDDAATYYCOLCNEPPTGAGTKLELK 110  
 DB 61 GVPARFSGSGSGTDFLTNIHPVEEDDAATYYCOHSRELPLTFGAGTKLELK 111

RESULT 10  
 KV3H\_MOUSE STANDARD; PRT; 111 AA.  
 ID KV3H\_MOUSE  
 AC P01660;

DT 21-JUL-1986 (rel. 01, Created)  
 DT 21-JUL-1986 (rel. 01, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 3741/TEPC 111.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: A01938; KYMS84.  
 DR HSSP: P80362; IWTL.  
 DR InterPro: IPR007110; Ig\_1like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.

FT DISULEID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 CC -1- MISCELLANEOUS: THE PC 3741 AND TERC 111 SEQUENCES ARE IDENTICAL.  
 DR PIR: A93204; KYMS37.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111  
 SEQUENCE 111 AA: 12099 MW: EC46C9D259213BE4 CRC64:

Query Match 78.3%; Score 455.5; DB 1; Length 111;  
 Best local Similarity 81.1%; Pred. No. 1.1e-38;  
 Matches 90; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKRASESVDSYGNFMHYQKPGQPKLLTYLASNL5 60  
 QY 60 GIPARFSGSGSDFTLNIHPVEEDAAATYYCOLCNEDEPTGAGTKLEK 110  
 DB 61 GIPARFSGSGSRDFTLTINIPVEADDAATYYCOQNEDEPTGAGTKLEK 111

RESULT 11  
 KV3J\_MOUSE STANDARD; PRT; 111 AA.  
 ID P01663;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 4050.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 (1)  
 SEQUENCE:  
 MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity".  
 RL Nature 276:785-790(1978).  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; IGV; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111  
 SEQUENCE 111 AA: 12005 MW: 39D87619313453CB CRC64:

Query Match 78.3%; Score 455.5; DB 1; Length 111;  
 Best local Similarity 82.0%; Pred. No. 1.1e-38;  
 Matches 91; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKRASESVDSYGNFMHYQKPGQPKLLTYLASNL5 60  
 QY 60 GIPARFSGSGSDFTLNIHPVEEDAAATYYCOLCNEDEPTGAGTKLEK 110  
 DB 61 GIPARFSGSGSRDFTLTINIPVEADDAATYYCOQNEDEPTGAGTKLEK 111

RESULT 12  
 KV3J\_MOUSE STANDARD; PRT; 111 AA.  
 ID P01673;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 2485/PC 4039.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 (1)  
 SEQUENCE:  
 MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity".  
 RL Nature 276:785-790(1978).  
 CC -1- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01939; KYMS85.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; IGV; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111  
 SEQUENCE 111 AA: 11986 MW: BF38C59AA7858467 CRC64:

Query Match 78.1%; Score 454.5; DB 1; Length 111;  
 Best local Similarity 82.9%; Pred. No. 1.3e-38;  
 Matches 92; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKRASESVDSYGNFMHYQKPGQPKLLTYLASNL5 60  
 QY 60 GIPARFSGSGSDFTLNIHPVEEDAAATYYCOLCNEDEPTGAGTKLEK 110  
 DB 61 GIPARFSGSGSRDFTLTINIPVEADDAATYYCOHSHNELPLTTCGAGTKLEK 111

RESULT 13  
 KV3J\_MOUSE STANDARD; PRT; 111 AA.  
 ID P01662;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-IIIT region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090.
RN [1]
RP MEDLINE=79012520; PubMed=99744;
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP MEDLINE=79073152; PubMed=103003;
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gathmann L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
-1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
HSSP: P01679; 2FRJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG_v.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;
Query Match 77.2%; Score 449.5; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 4,2e-38;
Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQOKPGQPKLLTYASNLNS 59
DB 1 NIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQOKPGQPKLLTYASNLNS 60
60 GIPARFSSGSGCTDFTLNIHVEEDATYYCOLCNEDEPPTFGAGTKLEK 110
61 GVPARFSSGSGRTDFTLTIDPEADATYYCQQNNEDPPTFGGCKLEIK 111
RESULT 14
KV3C_MOUSE STANDARD; PRT; 131 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IIIT region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).

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RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: B90412; KVM5M6.
DR HSSP: P01679; 2FRJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG_v.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-IIIT REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 77.1%; Score 448.5; DB 1; Length 131;
Best Local Similarity 80.2%; Pred. No. 6,4e-38;
Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQOKPGQPKLLTYASNLNS 59
DB 21 NIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQOKPGQPKLLTYASNLNS 80
60 GIPARFSSGSGCTDFTLNIHVEEDATYYCOLCNEDEPPTFGAGTKLEK 110
81 GVPARFSSGSGRTDFTLTIDPEADATYYCQQNNEDPPTFGGCKLEIK 131
RESULT 15
KV3C_MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IIIT region MOPC 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.E.;
RT "Mechanism of antibody synthesis: size differences between mouse
RT kappa chains."
RL Science 155:465-467(1967).
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR HSSP: P01679; 2FRJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.

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DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE: 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111  
 SQ SEQUENCE 111 AA: 11904 MW: 4FE7ABC9DF0FC125 CRC64;

Query Match 74.8%; Score 435.5; DB 1; Length 111;  
 Best Local Similarity 76.6%; Pred. No. 1e-36;  
 Matches 85; Conservative 10; Mismatches 15; Indels 1; Gaps 1;  
 1 DIVLTNSPASTAVSLGQRATISCKASQSVYDGDSDYM-WYQOKPGOPPKLTYAASNLES 59  
 1 DIVLTQSPASTAVSLGQRATISCRASESYDNGSISFMNWFQOKPGOPPKLTYAASNOGS 60  
 60 GIPARFSGSGSTDFTLNIHPVEEDATYYCQLCNEDEPTEGAGTKLELK 110  
 61 GVPARFSGSGSGSTDFSLNIHPMEEDDTAMVFCQSKREVWTFGGTKLEIK 111

Search completed: September 13, 2003, 07:52:47  
 Job time : 24 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:46:55 : Search time 84 Seconds  
(without alignments)  
337.926 Million cell updates/sec

Title: US-09-759-112a-24  
Perfect score: 582  
Sequence: 1 DIVLTNSPASPASLAVSLGCRAT.....CQLCNDDPPTFGAGTKLELK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Database: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_plant:\*  
10: SP\_rodent:\*  
11: SP\_virus:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467.5	80.3	111	11	Q920E9
2	413.5	71.0	103	11	Q9JL80
3	352.5	60.6	108	4	Q9UL70
4	348.5	59.9	108	4	Q9UL79
5	346	59.5	109	4	Q9UL78
6	342	58.8	108	11	Q9UL77
7	341.5	58.7	108	4	Q9UL77
8	341.5	58.7	107	4	Q9NEK1
9	341	58.6	107	4	Q9NEK1
10	340	58.4	112	11	Q9K1F2
11	338.5	58.2	108	4	Q9UL83
12	335	57.6	109	4	Q9UL85
13	335	57.6	112	11	Q9K1F3
14	334	57.4	112	11	Q9K1F3
15	334	57.4	239	4	Q9K1F3
16	330	56.7	114	11	Q9K1F1

17	327	56.2	239	11	Q9VC55	Q9VC55 mus musculus
18	325.5	55.9	114	4	Q9UL80	Q9UL80 homo sapien
19	325	55.8	107	4	Q9UL81	Q9UL81 homo sapien
20	324	55.7	239	4	Q9NEK0	Q9NEK0 homo sapien
21	321.5	55.2	108	11	Q9UL70	Q9UL70 mus musculus
22	314	54.0	106	5	Q9UL10	Q9UL10 schistosoma
23	313.5	53.9	214	11	Q9RIAS	Q9RIAS mus musculus
24	312	53.6	239	11	Q9KOF8	Q9KOF8 mus musculus
25	311	53.4	109	4	Q9UL86	Q9UL86 homo sapien
26	311	53.4	112	11	Q9K1F0	Q9K1F0 mus musculus
27	309.5	53.2	107	11	Q9ERT9	Q9ERT9 mus musculus
28	308	52.9	134	11	Q9VDD0	Q9VDD0 mus musculus
29	306.5	52.7	234	11	Q9LWF8	Q9LWF8 mus musculus
30	305.5	52.5	234	11	Q9KOF2	Q9KOF2 mus musculus
31	305	52.4	104	11	Q9UL82	Q9UL82 mus musculus
32	305	52.4	235	11	Q9LW12	Q9LW12 mus musculus
33	304.5	52.3	218	11	Q9ZS51	Q9ZS51 mus musculus
34	301.5	51.8	99	11	Q9UL74	Q9UL74 mus musculus
35	299.5	51.5	233	11	Q9LWS9	Q9LWS9 mus musculus
36	294.5	50.6	234	11	Q9VCP0	Q9VCP0 mus musculus
37	293.5	50.4	298	11	Q9QYF0	Q9QYF0 mus musculus
38	291.5	50.1	109	11	Q9ZDE6	Q9ZDE6 mus musculus
39	289.5	49.7	107	11	Q9JL84	Q9JL84 mus musculus
40	288.5	49.6	116	4	Q96PF6	Q96PF6 homo sapien
41	288.5	49.6	234	11	Q9R028	Q9R028 mus musculus
42	286.5	49.2	97	11	Q9JL76	Q9JL76 mus musculus
43	283.5	48.7	101	11	Q9JL78	Q9JL78 mus musculus
44	280	48.1	148	11	Q9K122	Q9K122 mus musculus
45	279.5	48.0	109	6	Q9N0W5	Q9N0W5 oryctolagus

## ALIGNMENTS

Q920E9	PRELIMINARY;	PRT;	111 AA.
Q920E9	Q920E9		
AC	Q920E9		
DT	01-DEC-2001 (TREMUREL 19, Created)		
DT	01-DEC-2001 (TREMUREL 19, Last sequence update)		
DE	01-MAR-2003 (TREMUREL 23, Last annotation update)		
DE	Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Atkin J.D., Iape A., Jennings I.G., Horvatis O., Cotton R.G.H.:		
RT	"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF307935; AL09419.1; -		
DR	InterPro: IPR007110; IG-LIKE.		
DR	InterPro: IPR003006; IG-MHC.		
DR	InterPro: IPR003596; IG-V.		
DR	SMART: SM00406; IGV; 1.		
DR	SMART: SM00406; IGV; 1.		
DR	PROSITE: PSS0835; IG-LIKE; 1.		
FT	NON_TER		
FT	NON_TER		
FT	SEQUENCE		
SQ	111 AA; 12046 MW; 1E46988AA6858526 CRC64;		
QY	Query Match		
QY	Best Local Similarity		
QY	Matches		
QY	93; Conservative		
QY	4; Mismatches		
QY	13; Indels		
QY	1; Gaps		
QY	1; Length		
QY	111; Pred. No. 1.5e-43;		
QY	1 DIVLTNSPASPASLAVSLGCRATISCKASQSVYDDDSYH-WIQQRGCPKLLTAASLDES 59		
QY	1 DIVLTNSPASPASLAVSLGCRATISCKASQSVYDDDSYH-WIQQRGCPKLLTAASLDES 60		
QY	60 GIPARFGSGSGTDFLTNIHPVEEDAAATYCCQLCNDDPPTFGAGTKLELK 110		

DB 61 GVPARFSGSGCTDFTLTINHPVEEDDAATYYCOHNSNELPYRTGGTKLEIK 111

## RESULT 2

09UL80 PRELIMINARY: PRT: 103 AA.

AC 09UL80;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin light chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-BALB/c;  
MEDLINE=20448942; PubMed=10992488;  
Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
"T-cell-dependent antibody response to the dominant epitope of  
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
with cardiac myosin.";  
RT Infect. Immun. 68:5803-5808(2000).  
RL EMBL; AF206026; AAF69324.1; -.  
DR HSSP; P80362; 1MTL.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 103  
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 71.0%; Score 413.5; DB 11; Length 103;  
Best Local Similarity 77.7%; Pred. No. 1.1e-37;  
Matches 80; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

OY 9 ASLAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSEGIPARESG 67  
RT fctus".  
RL 1 ASLAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSEGIPARESG 60  
OY 68 SSGTDFTLNHPVEEDDAATYYCOLCNEDEPPTFGAGTKLEIK 110  
61 SSGTDFTLNHPVEEDDAATYYCOLCNEDEPPTFGAGTKLEIK 103

09UL70 PRELIMINARY: PRT: 108 AA.

AC 09UL70;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
"Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus".  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL EMBL; AF035044; AAD56280.1; -.

DR HSSP; P01607; 1RET.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 60.6%; Score 352.5; DB 4; Length 108;  
Best Local Similarity 61.3%; Pred. No. 5.7e-31;  
Matches 68; Conservative 16; Mismatches 22; Indels 5; Gaps 2;

OY 1 DIVLTNSPASILAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSE 59  
1 DIVLTNSPASILAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSE 56  
DB 57 GVPARFSGSGCTDFTLTINHPVEEDDAATYYCOHNSNELPYRTGGTKLEIK 107

## RESULT 4

09UL79 PRELIMINARY: PRT: 108 AA.

AC 09UL79;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
"Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus".  
RL 1 DIVLTNSPASILAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSE 59  
1 DIVLTNSPASILAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSE 56  
OY 60 GIPARFSGSGCTDFTLTINHPVEEDDAATYYCOLCNEDEPPTFGAGTKLEIK 110  
61 GIPARFSGSGCTDFTLTINHPVEEDDAATYYCOLCNEDEPPTFGAGTKLEIK 107

DR HSSP; P01607; 1RET.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 59.9%; Score 348.5; DB 4; Length 108;  
Best Local Similarity 61.3%; Pred. No. 1.6e-30;  
Matches 68; Conservative 15; Mismatches 23; Indels 5; Gaps 2;

OY 1 DIVLTNSPASILAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSE 59  
1 DIVLTNSPASILAVSLGCRATISCKASQSYVDGDSYM-WYQKPGOPPKLLTYAASNLSE 56  
DB 57 GVPARFSGSGCTDFTLTINHPVEEDDAATYYCOHNSNELPYRTGGTKLEIK 107

## RESULT 5

09UL78 PRELIMINARY: PRT: 109 AA.

```
AC Q9UL78;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DR 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP: P80362; IWTI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; Ig_v.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 109 AA; 11646 MW; 5F675C52EC7E197 CRC64;
SQ
Query Match 59.5%; Score 346; DB 4; Length 109;
Best Local Similarity 62.2%; Pred. No. 3e-30;
Matches 69; Conservative 14; Mismatches 24; Indels 4; Gaps 2;
OY 1 DIVLTNSPASIYSLVSGRATISCKASQSVYDGDGYM-WYQKPGQPKLLTYAASNLES 59
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSV--SSYLAWYQKKGAKPRLITYGASSRAT 57
OY 60 GIPARFSGSGSGTFTLNHPVEEDATYYCQLCNEDPPTFGAGTKLEIK 110
DB 58 GIPDRFSGSGSGTFTLTISRLEPEDCAVYICQYGGSPITFGGTRVEIK 108
RESULT 6
O8VC16 PRELIMINARY; PRT; 238 AA.
ID O8VC16;
DC 08VC16;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DR 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019760; AAH19760.1;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; Ig_v.
DR PROSITE: PSS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match 58.8%; Score 342; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 2.2e-29;
Matches 68; Conservative 14; Mismatches 28; Indels 2; Gaps 2;
```

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OY 1 DIVLTNSPASIYSLVSGRATISCKASQSVYDGDGYM-WYQKPGQPKLLTYAASNLE 58
DB 20 DVVMTQTPSLPSVLGGQASISCRSSQSVHNSNNTLHWLQKPGQPKLLITYASNR 79
OY 59 SGIPARFSGSGSGTFTLNHPVEEDATYYCQLCNEDPPTFGAGTKLEIK 110
DB 80 SGVDRFSGSGSGTFTLTISRLEPEDLGVYFCQSSTHVPPTFGGTRVEIK 131
RESULT 7
O9UL77 PRELIMINARY; PRT; 108 AA.
ID O9UL77;
AC Q9UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DR 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig_v.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
SQ
Query Match 58.7%; Score 341.5; DB 4; Length 108;
Best Local Similarity 60.4%; Pred. No. 9.2e-30;
Matches 67; Conservative 17; Mismatches 22; Indels 5; Gaps 2;
OY 1 DIVLTNSPASIYSLVSGRATISCKASQSVYDGDGYM-WYQKPGQPKLLTYAASNLES 59
DB 1 DIQWTQSPSSIASVSGDRVTITCRASQSI---SSYLAWYQKKGAKPRLITYAASIS 56
OY 60 GIPARFSGSGSGTFTLNHPVEEDATYYCQLCNEDPPTFGAGTKLEIK 110
DB 57 GVPDRFSGSGSGTFTLTISRLEPEDATYYCQSYSTSWTFGEGTRVEIK 107
RESULT 8
O8NEK1 PRELIMINARY; PRT; 234 AA.
ID O8NEK1;
AC O8NEK1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DR 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC030813; AAH30813.1;
Query Match 58.8%; Score 342; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 2.2e-29;
Matches 68; Conservative 14; Mismatches 28; Indels 2; Gaps 2;
```

DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig: 2.  
 DR SMART: SM00407; IGH1.1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 SO SEQUENCE 234 AA; 25530 MW; 63168DEFD132F8 CRC64;

Query Match 58.7%; Score 341.5; DB 4; Length 234;  
 Best Local Similarity 60.0%; Pred. No. 2.4e-29;  
 Matches 66; Conservative 18; Mismatches 23; Indels 3; Gaps 1;

QY 1 DIVLTNSPASTLAVSLGQRTATSCASQSYVDGDSYMWYQKPGQPKLTLYAASNLK 60  
 DB 21 EIVMTQSPATLSVSGEERATLSCRASQSYT---SNLAWYQTPGQSPRLVITGASSRASG 77  
 61 IPARFSGSGSGTDFTLNHPVEEDAAATYVYCOLCNEDEPPTFGAGTKLELK 110  
 78 VPARFSGSGSGTDFTLTSLQSEDPFAVYVYCOQYKMKWPTFGGTRKLDIK 127

## RESULT 9

ID 096SA9 PRELIMINARY; PRT; 107 AA.

AC 096SA9  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain  
 DE Variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mysin  
 RT antibody V region genes.";  
 RT J. Immunol. 161:2020-2031(1998).  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL: U96396; AAB68785.1; -  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 SO SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;

Query Match 58.6%; Score 341; DB 4; Length 107;  
 Best Local Similarity 61.3%; Pred. No. 1e-29;  
 Matches 68; Conservative 18; Mismatches 19; Indels 6; Gaps 3;

QY 1 DIVLTNSPASTLAVSLGQRTATSCASQSYVDGDSYMWYQKPGQPKLTLYAASNLK 59  
 DB 1 DIOMTQSPATLSVSGEERATLSCRASQSYT---SSYLMWYQKPGKAPRLITLYAASNLK 56  
 60 GIPARFSGSGSGTDFTLNHPVEEDAAATYVYCOLCNEDEPPTFGAGTKLELK 110  
 57 GVPARFSGSGSGTDFTLTSLQSEDPFAVYVYCOQYKMKWPTFGGTRKLDIK 106

RESULT 10  
 ID 08K1F2 PRELIMINARY; PRT; 112 AA.

AC 08K1F2;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RT "Innate proteolytic antibodies: failed D-VIPase response to the D-  
 RT entantlomer of VIP and identification of L-VIPase VL domains.";  
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF516283; AAM64201.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00409; IG: 1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 SO SEQUENCE 112 AA; 11953 MW; 4716B87FAD8543ED CRC64;

Query Match 58.4%; Score 340; DB 11; Length 112;  
 Best Local Similarity 63.1%; Pred. No. 1.4e-29;  
 Matches 70; Conservative 12; Mismatches 23; Indels 6; Gaps 2;

QY 1 DIVLTNSPASTLAVSLGQRTATSCASQSYVDGDSYMWYQKPGQPKLTLYAASNLK 59  
 DB 1 DIVLTQSPATLSVSGEERATLSCRASQSYT---SYMHWYQKPGKAPRLITLYAASNLK 55  
 60 GIPARFSGSGSGTDFTLNHPVEEDAAATYVYCOLCNEDEPPTFGAGTKLELK 110  
 56 GVPARFSGSGSGTDFTLTSLQSEDPFAVYVYCOQYKMKWPTFGGTRKLDIK 106

RESULT 11  
 ID 09UL83 PRELIMINARY; PRT; 108 AA.

AC 09UL83;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035031; AAD56267.1; -  
 DR HSP: P80362; 1M7L.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 SO SEQUENCE 108 AA; 11080 MW; 4B43E9C5B577F16 CRC64;

Seq	Sequence	108 AA	11834 MW	9F9C5A92EEA96EEA	CRC64
SO	SEQUENCE	108 AA	11834 MW	9F9C5A92EEA96EEA	CRC64
QY	Query Match	58.2%	Score 338.5	DB 4	Length 108
DB	Best Local Similarity	60.9%	Pred. No. 2e-29		
Matches	67	Conservative	16	Mismatches	24
				Indels	3
				Gaps	1
QY	1 DIVLTNSPASLAVSLGCRATISCKRASQSVDDYDGSYMMYQOKPGQPPRLTYTAASNLESG 60				
DB	1 EIVMTQSPATLSVSGERATLSCRASQSV---SSNLAWYQOKPGQAPRLTYGASTRATG 57				
QY	61 IPARFSSGSGTDFLTINHPVEEDPAAYYCOLCNEPPTGAGTKLEK 110				
DB	58 IPARFSSGSGTDFLTITSSQLQFEDFAAYYCOHYNNMFTTGPGRKVIDK 107				
RESULT 12					
QY	09UL85				
ID	09UL85	PRELIMINARY	PRT	109 AA	
AC	09UL85				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DE	01-MAR-2003 (TREMBlrel. 23, Last annotation update)				
DE	Myosin-reactive immunoglobulin kappa chain variable region (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98277139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RT	fetus.";				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL: AF035029; AAD56265.1; -.				
DR	HSSP: P80362; IWL.				
DR	InterPro: IPR007110; Iq-1like.				
DR	InterPro: IPR003006; Iq_MHC.				
DR	InterPro: IPR003596; Iq_v.				
DR	Pfam: PF00047; Iq_1.				
DR	SMART: SM00406; Igv.1.				
DR	PROSITE: PS50835; Iq_LIKE; 1.				
FT	NON_TER	1			
FT	NON_TER	109			
FT	NON_TER	109			
QY	SEQUENCE	109 AA	11761 MW	FBI43E7C7AFACC	CRC64
QY	Query Match	57.6%	Score 335	DB 4	Length 109
DB	Best Local Similarity	60.4%	Pred. No. 4.8e-29		
Matches	67	Conservative	16	Mismatches	24
				Indels	4
				Gaps	2
QY	1 DIVLTNSPASLAVSLGCRATISCKRASQSVDDYDGSYMMYQOKPGQPPRLTYTAASNLESG 60				
DB	1 EIVMTQSPATLSVSGERATLSCRASQSV---SSNLAWYQOKPGQAPRLTYGASTRATG 57				
QY	61 IPARFSSGSGTDFLTINHPVEEDPAAYYCOLCNEPPTGAGTKLEK 110				
DB	58 IPARFSSGSGTDFLTITSSQLQFEDFAAYYCOHYNNMFTTGPGRKVIDK 108				
RESULT 13					
QY	08KLF3				
ID	08KLF3	PRELIMINARY	PRT	112 AA	
AC	08KLF3				
DT	01-OCT-2002 (TREMBlrel. 22, Created)				
DT	01-OCT-2002 (TREMBlrel. 22, Last sequence update)				
DE	01-MAR-2003 (TREMBlrel. 23, Last annotation update)				
DE	Anti-VIPase light chain variable region (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
OX	NBI_TaxID=10090;				

Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
1	57.6%	67	335	DB 11	112	4	1
2	60.9%	10	5e-29				
3	67	Conservative	10	Mismatches	29		
4	67	Conservative	17	Mismatches	26		
5	67	Conservative	17	Mismatches	26		
6	67	Conservative	17	Mismatches	26		
7	67	Conservative	17	Mismatches	26		
8	67	Conservative	17	Mismatches	26		
9	67	Conservative	17	Mismatches	26		
10	67	Conservative	17	Mismatches	26		
11	67	Conservative	17	Mismatches	26		
12	67	Conservative	17	Mismatches	26		
13	67	Conservative	17	Mismatches	26		
14	67	Conservative	17	Mismatches	26		
15	67	Conservative	17	Mismatches	26		
16	67	Conservative	17	Mismatches	26		
17	67	Conservative	17	Mismatches	26		
18	67	Conservative	17	Mismatches	26		
19	67	Conservative	17	Mismatches	26		
20	67	Conservative	17	Mismatches	26		
21	67	Conservative	17	Mismatches	26		
22	67	Conservative	17	Mismatches	26		
23	67	Conservative	17	Mismatches	26		
24	67	Conservative	17	Mismatches	26		
25	67	Conservative	17	Mismatches	26		
26	67	Conservative	17	Mismatches	26		
27	67	Conservative	17	Mismatches	26		
28	67	Conservative	17	Mismatches	26		
29	67	Conservative	17	Mismatches	26		
30	67	Conservative	17	Mismatches	26		
31	67	Conservative	17	Mismatches	26		
32	67	Conservative	17	Mismatches	26		
33	67	Conservative	17	Mismatches	26		
34	67	Conservative	17	Mismatches	26		
35	67	Conservative	17	Mismatches	26		
36	67	Conservative	17	Mismatches	26		
37	67	Conservative	17	Mismatches	26		
38	67	Conservative	17	Mismatches	26		
39	67	Conservative	17	Mismatches	26		
40	67	Conservative	17	Mismatches	26		
41	67	Conservative	17	Mismatches	26		
42	67	Conservative	17	Mismatches	26		
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58	67	Conservative	17	Mismatches	26		
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60	67	Conservative	17	Mismatches	26		
61	67	Conservative	17	Mismatches	26		
62	67	Conservative	17	Mismatches	26		





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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:55:26 ; Search time 54 Seconds  
(without alignments)  
297.229 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582  
Sequence: 1 DIVLNSPASTSLAVSLGORAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 541936  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published\_Applications-AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	110	11	US-09-759-112a-24
2	537.5	92.4	132	10	US-09-879-461-2
3	528.5	90.8	238	15	US-10-216-484-11
4	526.5	90.5	238	10	US-09-903-327A-4
5	505.5	86.9	112	15	US-10-194-975-115
6	503.5	86.5	106	9	US-09-802-077-6
7	503.5	86.5	106	9	US-09-802-096-6
8	503.5	86.5	106	11	US-09-925-179-6
9	491.5	84.5	111	9	US-09-802-077-2
10	491.5	84.5	111	9	US-09-802-096-2
11	491.5	84.5	111	11	US-09-925-179-2
12	490	84.2	112	12	US-10-160-506-81
13	487.5	83.8	238	15	US-10-216-484-34
14	485.5	83.4	111	9	US-09-920-171-5
15	485.5	83.4	111	12	US-10-113-996-5

16	476.5	81.9	238	15	US-10-216-484-52	Sequence 52, Appl
17	475.5	81.7	238	15	US-10-216-484-109	Sequence 109, App
18	475.5	81.7	271	12	US-10-053-590-12	Sequence 12, Appl
19	473.5	81.7	271	15	US-10-207-655-12	Sequence 12, Appl
20	469.5	80.7	131	10	US-09-879-461-58	Sequence 14, Appl
21	463.5	79.6	131	10	US-09-879-461-14	Sequence 58, Appl
22	461.5	79.3	112	9	US-09-810-502-37	Sequence 37, Appl
23	459.5	79.0	112	9	US-09-144-886-80	Sequence 80, Appl
24	453.5	77.9	218	15	US-10-171-452A-39	Sequence 39, Appl
25	453.5	77.9	218	15	US-10-171-452A-45	Sequence 45, Appl
26	453.5	77.9	218	15	US-10-171-452A-51	Sequence 51, Appl
27	453.5	77.9	218	15	US-10-171-452A-57	Sequence 57, Appl
28	453.5	77.9	238	15	US-10-171-452A-38	Sequence 38, Appl
29	453.5	77.9	238	15	US-10-171-452A-44	Sequence 44, Appl
30	453.5	77.9	238	15	US-10-171-452A-50	Sequence 50, Appl
31	453.5	77.9	238	15	US-10-171-452A-56	Sequence 56, Appl
32	451	77.4	112	12	US-10-160-506-82	Sequence 82, Appl
33	450.5	77.4	112	10	US-09-144-886-87	Sequence 87, Appl
34	448.5	77.1	112	10	US-09-144-886-84	Sequence 84, Appl
35	448.5	77.1	129	9	US-09-839-447A-2	Sequence 2, Appl
36	448.5	77.1	129	15	US-10-153-271-2	Sequence 2, Appl
37	446.5	76.7	238	15	US-10-216-484-129	Sequence 129, App
38	444.5	76.4	112	10	US-09-144-886-85	Sequence 85, Appl
39	444	76.3	110	10	US-09-974-052-13	Sequence 13, Appl
40	444	76.3	110	10	US-09-974-051-13	Sequence 13, Appl
41	444	76.3	110	11	US-09-974-516-13	Sequence 13, Appl
42	443.5	76.2	112	10	US-09-144-886-81	Sequence 81, Appl
43	443.5	76.2	134	9	US-09-881-823-2	Sequence 2, Appl
44	443.5	76.2	238	15	US-10-216-484-131	Sequence 131, App
45	442.5	76.0	112	10	US-09-144-886-86	Sequence 86, Appl

## ALIGNMENTS

US-09-759-112a-24	US-09-759-112a-24
Sequence 24, Application US/09759112A	
Publication No. US20030100741A1	
GENERAL INFORMATION:	
APPLICANT: Mueller, Sybille	
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LI	
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1E7, AN ANTI-IDIOTYPIC ANTIBODY REACTI	
TITLE OF INVENTION: ANTIBODIES	
FILE REFERENCE: 200-013	
CURRENT APPLICATION NUMBER: US/09/759, 112A	
CURRENT FILING DATE: 2001-01-11	
NUMBER OF SEQ ID NOS: 38	
SOFTWARE: PatentIn version 3.0	
SEQ ID NO 24	
LENGTH: 110	
TYPE: PRT	
ORGANISM: mouse	
US-09-759-112a-24	
Query Match	100.0%; Score 582; DB 11; Length 110;
Best Local Similarity	100.0%; Pred. No. 1.8e-49;
Matches 110; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 DIVLNSPASTSLAVSLGORATISCKASQSDYGDSDSYMYQKPGOPPKLLTYAASNLSESG 60
DB	1 DIVLNSPASTSLAVSLGORATISCKASQSDYGDSDSYMYQKPGOPPKLLTYAASNLSESG 60
QY	61 IPARSGSGSGDTFLNTHIPVEEDATYYCOLCNEDEPTFGAGTKLELK 110
DB	61 IPARSGSGSGDTFLNTHIPVEEDATYYCOLCNEDEPTFGAGTKLELK 110
RESULT 2	
US-09-879-461-2	
Sequence 2, Application US/09879461	
Publication No. US20020193575A1	

```

: GENERAL INFORMATION:
: APPLICANT: Holmes, Stephen D.
: Gross, Mitchell S.
: Sylvester, Daniel R.
: TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
: Treatment of IL4 Mediated Disorders
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: Corporate Intellectual Property, UW2220 - 709
: Swedeland Rd.
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-2799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/879,461
: FILING DATE: 12-Jun-2001
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/612,929
: FILING DATE: <unknown>
: APPLICATION NUMBER: US 08/136,783
: FILING DATE: 14-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Sutton, Jeffrey A.
: REGISTRATION NUMBER: 34,028
: REFERENCE/DOCKET NUMBER: P50186-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 270-5024
: TELEFAX: (215) 270-5090
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 132 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
: US-09-879-461-2
:
: Query Match 92.4%: Score 537.5; DB 10; Length 132;
: Best Local Similarity 93.7%: Pred. No. 4.7e-45;
: Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
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: 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQOKPGQPKLLTYASNLES 59
: |||||
: 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYMWYQOKPGQPKLLTYASNLES 80
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: 60 GIPARFSGSGSGTFTLNINHPVEEDDATYTCQLCNEPPTFGAGTKLEK 110
: |||||
: 81 GIPARFSGSGSGTFTLNINHPVEEDDATYTCQSDNEPPTFGGKTLEIK 131
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: RESULT 3
: US-10-216-484-11
: Sequence 11, Application US/10216484
: Publication NO. US20030103976A1
: GENERAL INFORMATION:
: APPLICANT: Serizawa, No. US20030103976A1ufusa
: APPLICANT: Haruyama, Hideyuki
: APPLICANT: Nakahara, Kaori
: APPLICANT: Tamaki, Ikuko
: APPLICANT: Takahashi, Tohru
: TITLE OF INVENTION: Anti-Fas Antibodies
: FILE REFERENCE: 980126CIP/HG
: CURRENT APPLICATION NUMBER: US/10/216,484
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: US/09/499,662

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: PRIOR FILING DATE: 2000-02-09
: PRIOR APPLICATION NUMBER: US 09/053,583
: PRIOR FILING DATE: 1998-04-01
: NUMBER OF SEQ ID NOS: 165
: SEQ ID NO 11
: LENGTH: 238
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-216-484-11

Query Match
Best Local Similarity 90.8%; Score 528.5; DB 15; Length 238;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIVTNSPASLAVSLGORATISCKASOSVDYDGDSTM-WYQKFGQPPKLLITYAASNLES 59
Db 21 DIVTOSPASLAVSLGORATISCKASOSVDYDGDSTMWYQKFGQPPKLLITYAASNLES 80
60 GIPARFSGSGGTDFTLNHPVEEEDATATYQCQCNEDPPTFGGKLEIK 110
81 GIPARFSGSGGTDFTLNHPVEEEDATATYQCQCNEDPPTFGGKLEIK 131

RESULT 4
US-09-903-327A-4
: Sequence 4, Application US/09903327A
: Patent No. US2002016433A1
: GENERAL INFORMATION:
: APPLICANT: Nemerow, Glen R.
: APPLICANT: Li, Erlingung
: TITLE OF INVENTION: BIOFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAA
: TITLE OF INVENTION: GENE
: FILE REFERENCE: 22908-1228
: CURRENT APPLICATION NUMBER: US/09/903,327A
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: 09/613,017
: PRIOR FILING DATE: 2000-07-10
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 238
: TYPE: PRT
: ORGANISM: Mouse
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (0)...(0)
: OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match
Best Local Similarity 90.5%; Score 526.5; DB 10; Length 238;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIVTNSPASLAVSLGORATISCKASOSVDYDGDSTM-WYQKFGQPPKLLITYAASNLES 59
Db 21 DIVTOSPASLAVSLGORATISCKASOSVDYDGDSTMWYQKFGQPPKLLITYAASNLES 80
60 GIPARFSGSGGTDFTLNHPVEEEDATATYQCQCNEDPPTFGGKLEIK 110
81 GIPARFSGSGGTDFTLNHPVEEEDATATYQCQCNEDPPTFGGKLEIK 131

RESULT 5
US-10-194-975-115
: Sequence 115, Application US/10194975
: Publication No. US20030039649A1
: GENERAL INFORMATION:
: APPLICANT: Foote, Jefferson
: TITLE OF INVENTION: Super Humanized Antibodies
: FILE REFERENCE: 501231.01
: CURRENT APPLICATION NUMBER: US/10/194,975
: CURRENT FILING DATE: 2002-10-10

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;; PRIOR APPLICATION NUMBER: US 60/305,111  
;; PRIOR FILING DATE: 2001-07-12  
;; NUMBER OF SEQ ID NOS: 122  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 115  
;; LENGTH: 112  
;; TYPE: PRT  
;; ORGANISM: Mus sp.  
US-10-194-975-115

Query Match 86.5%; Score 505.5; DB 15; Length 112;  
Best Local Similarity 88.3%; Pred. No. 7.6e-42;  
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDSTW-WYQKRGKGPPLKLTAAASNLES 59  
Db 1 DIVLTQSPASTAVSLGKATISCKASQSVYDGDSTWYQKRGKGPPLKLTAAASNLES 60

60 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 110  
61 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 111

RESULT 6  
US-09-802-077-6  
;; Sequence 6, Application US/09802077  
;; Patent No. US20010033842A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jardiou, Paula M.  
;; APPLICANT: Presta, Leonard G.  
;; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
;; FILE REFERENCE: P0718P2C3US  
;; CURRENT APPLICATION NUMBER: US/09/802,077  
;; CURRENT FILING DATE: 2001-03-08  
;; PRIOR APPLICATION NUMBER: US 08/405,617  
;; PRIOR FILING DATE: 1995-03-15  
;; PRIOR APPLICATION NUMBER: US 08/185,899  
;; PRIOR FILING DATE: 1994-01-26  
;; PRIOR APPLICATION NUMBER: PCT/US92/06860  
;; PRIOR FILING DATE: 1992-08-14  
;; PRIOR APPLICATION NUMBER: US 07/879,495  
;; PRIOR FILING DATE: 1992-05-07  
;; PRIOR APPLICATION NUMBER: US 07/744,768  
;; PRIOR FILING DATE: 1991-08-14  
;; NUMBER OF SEQ ID NOS: 64  
;; SEQ ID NO 6  
;; LENGTH: 106  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-802-077-6

Query Match 86.5%; Score 503.5; DB 9; Length 106;  
Best Local Similarity 93.4%; Pred. No. 7.6e-42;  
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDSTW-WYQKRGKGPPLKLTAAASNLES 59  
Db 1 DIVLTQSPASTAVSLGKATISCKASQSVYDGDSTWYQKRGKGPPLKLTAAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 105  
Db 61 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 106

RESULT 7  
US-09-802-096-6  
;; Sequence 6, Application US/09802096  
;; Patent No. US20010033839A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jardiou, Paula M.  
;; APPLICANT: Presta, Leonard G.  
;; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
;; FILE REFERENCE: P0718P2C3US

;; CURRENT APPLICATION NUMBER: US/09/802,096  
;; CURRENT FILING DATE: 2001-03-08  
;; PRIOR APPLICATION NUMBER: US 08/405,617  
;; PRIOR FILING DATE: 1995-03-15  
;; PRIOR APPLICATION NUMBER: US 08/185,899  
;; PRIOR FILING DATE: 1994-01-26  
;; PRIOR APPLICATION NUMBER: PCT/US92/06860  
;; PRIOR FILING DATE: 1992-08-14  
;; PRIOR APPLICATION NUMBER: US 07/879,495  
;; PRIOR FILING DATE: 1992-05-07  
;; PRIOR APPLICATION NUMBER: US 07/744,768  
;; PRIOR FILING DATE: 1991-08-14  
;; NUMBER OF SEQ ID NOS: 64  
;; SEQ ID NO 6  
;; LENGTH: 106  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-802-096-6

Query Match 86.5%; Score 503.5; DB 9; Length 106;  
Best Local Similarity 93.4%; Pred. No. 7.6e-42;  
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDSTW-WYQKRGKGPPLKLTAAASNLES 59  
Db 1 DIVLTQSPASTAVSLGKATISCKASQSVYDGDSTWYQKRGKGPPLKLTAAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 105  
Db 61 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 106

RESULT 8  
US-09-925-179-6  
;; Sequence 6, Application US/09925179  
;; Publication No. US20030044858A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jardiou, Paula M.  
;; APPLICANT: Presta, Leonard G.  
;; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)  
;; FILE REFERENCE: P0718P2C3US  
;; CURRENT APPLICATION NUMBER: US/09/925,179  
;; CURRENT FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 08/466,163  
;; PRIOR FILING DATE: 1995-06-06  
;; PRIOR APPLICATION NUMBER: US 08/405,617  
;; PRIOR FILING DATE: 1995-03-15  
;; PRIOR APPLICATION NUMBER: US 08/185,899  
;; PRIOR FILING DATE: 1994-01-26  
;; PRIOR APPLICATION NUMBER: PCT/US92/06860  
;; PRIOR FILING DATE: 1992-08-14  
;; PRIOR APPLICATION NUMBER: US 07/879,495  
;; PRIOR FILING DATE: 1992-05-07  
;; PRIOR APPLICATION NUMBER: US 07/744,768  
;; PRIOR FILING DATE: 1991-08-14  
;; NUMBER OF SEQ ID NOS: 68  
;; SEQ ID NO 6  
;; LENGTH: 106  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-925-179-6

Query Match 86.5%; Score 503.5; DB 11; Length 106;  
Best Local Similarity 93.4%; Pred. No. 7.6e-42;  
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db 1 DIVLTQSPASTAVSLGKATISCKASQSVYDGDSTWYQKRGKGPPLKLTAAASNLES 60

QY 60 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 105  
Db 61 GIPARFSGSGSGTDFLTNIHIVPEEEDATATYCCQNSNEDPPTFGAGT 106

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RESULT 9
US-09-802-077-2
; Sequence 2, Application US/09802077
; Patent No. US2001003842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-2

Query Match      84.5%: Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%: Pred. No. 1.2e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTSLAVSGORATISCKASQSYVDGDSYM-WYQOKPCQPPKLLTYAASNL5S 59
DB 1 DIVLTQSPASTSLAVSLGQRTATISCKASQSYVDGDSYMMNYQOKPCQPPKLLTYAASYLGS 60
OY 60 GIPARFSGSGCTDFTLNINHPVEEDDAATYYCQLCNEDPPTFGAGTKLELK 110
DB 61 EIPARFSGSGCTDFTLNINHPVEEDDAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 10
US-09-802-096-2
; Sequence 2, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-2

Query Match      84.5%: Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%: Pred. No. 1.2e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
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Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTSLAVSGORATISCKASQSYVDGDSYM-WYQOKPCQPPKLLTYAASNL5S 59
DB 1 DIVLTQSPASTSLAVSLGQRTATISCKASQSYVDGDSYMMNYQOKPCQPPKLLTYAASYLGS 60
OY 60 GIPARFSGSGCTDFTLNINHPVEEDDAATYYCQLCNEDPPTFGAGTKLELK 110
DB 61 EIPARFSGSGCTDFTLNINHPVEEDDAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 11
US-09-925-179-2
; Sequence 2, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C3US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-2

Query Match      84.5%: Score 491.5; DB 11; Length 111;
Best Local Similarity 88.3%: Pred. No. 1.2e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTSLAVSGORATISCKASQSYVDGDSYM-WYQOKPCQPPKLLTYAASNL5S 59
DB 1 DIVLTQSPASTSLAVSLGQRTATISCKASQSYVDGDSYMMNYQOKPCQPPKLLTYAASYLGS 60
OY 60 GIPARFSGSGCTDFTLNINHPVEEDDAATYYCQLCNEDPPTFGAGTKLELK 110
DB 61 EIPARFSGSGCTDFTLNINHPVEEDDAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 12
US-10-160-506-81
; Sequence 81, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 02:30:53 ; Search time 282 Seconds  
(without alignments)  
3158.917 Million cell updates/sec

Title: US-09-759-112a-23

Perfect score: 330  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	100.0	330	24	AA148660
2	330	100.0	330	24	AA148661
3	294.6	89.3	336	16	AA083490
4	294.6	89.3	336	20	AA083490
5	294.6	89.3	336	20	AA083490
6	293	88.8	333	21	AA258690
7	293	88.8	333	21	AA244232
8	293	88.8	333	21	AA244232
				19	AAV70130

9	293	88.8	714	21	AAA72109
10	293	88.8	714	21	AAA11547
11	293	88.8	714	21	AB145926
12	293	88.8	714	24	AB148669
13	293	88.8	925	21	AA258663
14	293	88.8	925	21	AA258664
15	293	88.8	925	21	AA244205
16	293	88.8	925	21	AA244205
17	288.2	87.3	333	15	AA065554
18	288.2	87.3	333	15	AA070372
19	286.6	86.8	333	24	ABR88124
20	286.6	86.8	831	24	AA029309
21	286.6	86.8	831	25	ABX12745
22	285	86.4	334	10	AA090492
23	285	86.4	333	14	AA036609
24	285	86.4	733	13	AA025658
25	285	86.4	780	10	AA090495
26	282.4	85.6	669	18	AA059338
27	280.8	85.1	900	11	AA004039
28	277	83.9	336	22	AA062145
29	275.4	83.5	768	19	AAV70076
30	275.4	83.5	768	21	AAV72126
31	275.4	83.5	768	21	AAV11564
32	275.4	83.5	768	24	AB145943
33	275.4	83.5	768	24	AB148686
34	273.8	83.0	309	21	AA258662
35	273.8	83.0	309	21	AA244204
36	272.2	82.5	768	19	AAV70075
37	272.2	82.5	768	19	AAV70078
38	272.2	82.5	768	21	AAV72125
39	272.2	82.5	768	21	AAV72125
40	272.2	82.5	768	21	AAV72125
41	272.2	82.5	768	21	AAV72125
42	272.2	82.5	768	21	AAV72125
43	272.2	82.5	768	24	AB145942
44	272.2	82.5	768	24	AB145942
45	272.2	82.5	768	24	AB148737

## ALIGNMENTS

RESULT 1	AA148660	standard; DNA; 330 BP.
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AC	AA148660	
DT	11-OCT-2002 (first entry)	
DE	Murine Mab 1F7 Light chain coding sequence.	
KW	Mouse: 1F7; antibody; Immune modulator; anti-HIV antibody; CDR;	
KW	complementarity determining region; framework-determining region;	
KW	FR; heavy chain; Light chain; HIV infection; gene; ss.	
OS	Mus sp.	
PN	WO200255668-A2.	
PD	18-JUL-2002.	
PF	11-JAN-2002; 2002WO-US00927.	
PR	11-JAN-2001; 2001US-0759112.	
PA	(IMMP-) IMMUPHERON INC.	
PI	Muller S, Kohler H;	
DR	WPI; 2002-590668/63.	
PT	New polynucleotide encoding a complementarity- or framework-determining	

CDNA encoding mouse  
Murine anti-Fas an  
Mouse humanised an  
Humanised anti-Fas  
Antibody 4H5 H cha  
Murine derived DNA  
Murine derived DNA  
Mouse anti-HIV mu5  
Anti HIV antibody  
DNA encoding mouse  
Human penton base  
DNA encoding mouse  
Gene fragment of 1  
Anti-CD4 antibody  
Mouse 0.5beta anti  
A V chl region gen  
MHI monoclonal ant  
Anti-leu 3a light  
Anti-SAF-1 monoclo  
Anti-Fas humanised  
DNA encoding human  
Humanised anti-Fas  
Humanised anti-Fas  
Humanised anti-Fas  
Antibody 4H5 L cha  
Murine derived DNA  
Humanised anti-Fas  
Humanised anti-Fas  
Humanised anti-Fas









0Y	238	CCTGTGGAGGAGAGATGCTCCATCCATTTACTGTGTAATGAGATCCTCC	237
Db	241	CCTGTGGAGGAGAGATGCTCCATCCATTTACTGTGTAATGAGATCCTCC	300
0Y	298	ACGTTGGTCTGGAGCAAGCTGAGCTGAAA	330
Db	301	ACGTTGGTGGAGCCACCAAGCTGGAATATCAAA	333
RESULT 7			
ID	AAZ44232		
XX	AAZ44232 standard: DNA: 333 BP.		
XX	AAZ44232:		
XX	AC		
XX	AAZ44232:		
DT	31-MAR-2000 (first entry)		
XX	Murine derived DNA fragment #6.		
XX	Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;		
KW	hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;		
XX	HIV infection; autoimmune disease; murine; ds.		
XX	Mus sp.		
OS			
XX	WO9961629-A1.		
PN			
XX	02-DEC-1999.		
PD			
XX	24-MAY-1999; 99WO-JP02711.		
PF			
XX	25-MAY-1998; 98JP-0159957.		
XX	26-MAY-1998; 98JP-0163023.		
XX	(ASAH ) ASAH KASEI KOGYO KK.		
PA	(ASAH ) ASAH MEDICAL CO LTD.		
PI	Ono M, Soka T, Morimoto I, Miyamura K;		
XX			
DR	WPI: 2000-086720/07.		
XX	P-PSDB: AAY51146.		
PT	Devices containing antibodies recognising CD4 or CD34 and their use for		
XX	the separation of CD4 or CD34 positive cells		
XX	Disclosure: Page 97-98; 111pp; Japanese.		
XX	This invention describes a novel device (I) for separating cluster		
XX	differentiation (CD)-positive cells using a recombinant (chimeric or		
XX	single-chain) antibody recognising CD4 or CD34. The devices are useful		
XX	for the separation of CD4 or CD34 positive cells, which is useful for		
XX	the collection of hematopoietic undifferentiated cells, elimination of		
XX	lymphocytes from cells to be used in bone marrow transplantation, the		
XX	detection of leukemic cells and the production of medicinal		
XX	compositions for the treatment of HIV infection and autoimmune diseases.		
XX	This sequence encodes a murine derived protein fragment which is used		
XX	to illustrate the method of the invention.		
XX	Sequence 333 BP; 87 A; 86 C; 84 G; 76 T; 0 other:		
0Y	Query Match	88.8%; Score 293; DB 21; Length 333;	
Db	Best Local Similarity	94.6%; Pred. No. 6; 6e-81;	
0Y	Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1		
0Y	1 GACATGTGCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCACC	60	
Db	1 GACATGTGCTGAGCCCAATCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCACC	60	
0Y	ATTCCTGCAAGGCGCAGCAAGTGTGATGATGAGTGATATATG--TGGTAC	117	
Db	61 ATTCCTGCAAGGCGCAGCAAGTGTGATGATGAGTGATATATGAACTGTGAC	120	

QY	118	CAACCAAAACAGAGAGAGCACC	CAAACTCCTACCTTGGCATCCAACTGTGAATCT	177
Db	121	CAACCAAAACAGAGAGAGCACC	CAAACTCCTCATCTATCTGTCATCCAATCTGAATCT	180
QY	178	GGGATCCACGACAGGTTT	AGTGGCAGTGGGTCGTGGGACAGACTTCACCTCAACATCAT	237
Db	181	GGGATCCACGACAGGTTT	AGTGGCAGTGGGTCGTGGGACAGACTTCACCTCAACATCAT	240
QY	238	CCGTGTGGAGAGAGAGAGATCT	CTCAACCTATTACTGTACGCTTTTGTAATGAGATCTTCCC	297
Db	241	CCGTGTGGAGAGAGAGATCT	CTCAACCTATTACTGTACGAAAGATGAGAGATCTTCCG	300
QY	298	ACGTTGGTGTCGGGACCAAGCTG	AGCGTGAAC	330
Db	301	ACGTTGGTGAGGACCAAGCTG	AGAAATCAAA	333
RESULT 8				
ID	AAV70130	standard; cDNA to mRNA; 714 BP.		
XX	AAV70130;			
AC	AAV70130;			
XX	25-MAR-2003 (updated)			
DT	15-MAR-1999 (first entry)			
DT	15-MAR-1999 (first entry)			
XX	Anti-Fas MAB HFE7A light chain cDNA.			
DE	HEF7A: monoclonal antibody; mouse; Fas; humanised antibody;			
XX	apoptosis; HFE7A: autoimmune disease; Hashimoto's disease;			
KW	systemic lupus erythematosus; graft versus host disease;			
KW	Sjogren syndrome; pernicious anaemia; Addison's disease;			
KW	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;			
KW	rheumatoid arthritis; autoimmune haemolytic anaemia;			
KW	myasthenia gravis; multiple sclerosis; Basedow's disease;			
KW	thrombopenia purpura; insulin-dependent diabetes; allergy;			
KW	atrophy; arteriosclerosis; myocarditis; cardiomyopathy;			
KW	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;			
KW	transplant rejection; therapy; ds.			
XX	Mus musculus.			
OS	Mus musculus.			
XX	Key	Location/Qualifiers		
FT	sig_peptide	1..60		
FT	mat_peptide	61..714		
FT		/*tag= a		
FT		/*tag= b		
XX	AU9859701-A.			
XX	08-OCT-1998.			
XX	30-MAR-1998;	98AU-0059701.		
XX	08-OCT-1997;	97JP-0276064.		
XX	01-APR-1997;	97JP-0082953.		
XX	25-JUN-1997;	97JP-0169088.		
XX	(SANY ) SANKYO CO LTD.			
PI	Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;			
PI	Masahiko O, Nobufusa S, Shin Y, Tohru T;			
XX	WPI: 1998-543440/01.			
XX	P-PSDB: AAM83042.			
XX	New antibodies and proteins bind conserved epitope of Fas antigen -			
XX	used to evaluate drugs in animal models and to treat Fas-associated			
XX	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,			
XX	myocarditis, hepatitis and AIDS			
XX	Reference Example 4; Page 188-189; 292pp; English.			



KM anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;  
 KM dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KM nephrotropic; antifertility; neuroprotective; antidiabetic; sclerotic;  
 KM hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;  
 KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KM Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KM multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN EP990663-AZ.  
 XX  
 XX 05-APR-2000.  
 PD  
 PF 29-SEP-1999; 99EP-0307711.  
 30-SEP-1998; 98JP-0276881.  
 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI: 2000-258930/23.  
 P-PSDB: AAM90898.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 PS  
 PS Example reference 4; Page 102-103; 263pp; English.  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
 CC antidiabetic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (II) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence encodes  
 CC a murine anti-Fas monoclonal antibody HFE7A light chain described in the  
 CC method of the invention.  
 CC  
 XX  
 SQ Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;

Query Match 88.8%; Score 293; DB 21; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 8, 5e-81;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

1 GACATTGTCGTCACCAATTCACACTTCTTGGCTGTCTCTAGGCGACAGGCCAC 60  
 61 GACATTGTCGTCACCAATTCACACTTCTTGGCTGTCTCTAGGCGACAGGCCAC 120

OY 61 ATCTCCTGCAGAGCCAGCCAAAGTGTGATTTGATGGTATGATG--TGTATC 117  
 DB 121 ATCTCCTGCAGAGCCAGCCAAAGTGTGATTTGATGGTATGATGATGACTGTAC 180  
 OY 118 CAACAGAAACAGAGAGAGCCAGCCAAAGTGTGATTTGATGGTATGATGATGACTGTAC 177  
 DB 181 CAACAGAAACAGAGAGAGCCAGCCAAAGTGTGATTTGATGGTATGATGATGACTGTAC 240  
 OY 178 GGGATCCAGAGCCAGGTTTATGTTAGTGGAGTGGTGGAGACAGCTTACACCTCAACATCCAT 237  
 DB 241 GGGATCCAGAGCCAGGTTTATGTTAGTGGAGTGGTGGAGACAGCTTACACCTCAACATCCAT 300  
 OY 238 CCTGTGAGAGAGAGAGAGTGTGCAACCTATTACTGACCTTGTATGAGATGATCCTGCC 297  
 DB 301 CCTGTGAGAGAGAGAGAGTGTGCAACCTATTACTGACCTTGTATGAGATGATCCTGCC 360  
 OY 298 ACGTTGCGTGTGAGAGAGAGAGTGTGCAACCTATTACTGACCTTGTATGAGATGATCCTGCC 330  
 DB 361 ACGTTGCGTGTGAGAGAGAGAGTGTGCAACCTATTACTGACCTTGTATGAGATGATCCTGCC 393

## RESULT 11

ABL45926 standard; cDNA; 714 BP.

ABL45926;

26-APR-2002 (first entry)

Mouse humanised anti-Fas antibody related cDNA SEQ ID NO 8.

Human: mouse; humanised anti-Fas antibody; Fas/Fas ligand;

light chain subunit; apoptosis; immunosuppressive; antiallergic;

autoimmune disease; allergy; atopic; ss.

Mus musculus.

JP2001342148-A.

11-DEC-2001.

28-MAR-2001; 2001JP-0093106.

29-MAR-2000; 2000JP-0090918.

(SANY ) SANKYO CO LTD.

WPI: 2002-145113/19.

P-PSDB; ABB74904.

Drug containing humanised anti-Fas antibody, used for preventing and

treating autoimmune diseases, allergy, and atopy -

Example 4 (Preparatory); Page 77-79; 194pp; Japanese.

The invention relates to a preventive or treating agent for diseases

caused by abnormality in Fas/Fas ligand system containing as the active

component an antibody having as the light chain subunit a polypeptide

containing residues 1-218 of one of 3, 239 residue amino acid sequences,

or residues 1-451 of one of 3, 470 residue amino acid sequences, all

fully defined in the specification and having an activity of combining

specifically with mammalian Fas and an activity of inducing apoptosis

in a cell expressing Fas. The agent has immunosuppressive and

antiallergic activity and is used for preventing and treating autoimmune

diseases, allergy, atopy and others.

Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;

Query Match 88.8%; Score 293; DB 24; Length 714;

Best Local Similarity 94.6%; Pred. No. 8, 5e-81;

Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

1 GACATTGTCGTCACCAATTCACACTTCTTGGCTGTCTCTAGGCGACAGGCCAC 60









GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 05:05:14 : Search time 2595 Seconds  
(without alignments)  
3090.743 Million cell updates/sec

Title: US-09-759-112a-23

Perfect score: 330  
Sequence: 1 gacatgtctcaccaatc.....ggaccaagctgagctgaaa 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	250.4	75.9	659	10 BF137298 601781658
2	249.8	75.7	407	10 AW988429 u908607.y
3	245	74.2	683	11 AF240172 Mus muscu
4	245	74.2	1108	12 BG969221 602835202

5	244.8	74.2	774	10 BF581989
6	244	73.9	76	12 BG965050
7	241.8	73.3	398	10 AA423447
8	241.8	73.3	643	14 BY733441
9	240.4	72.8	831	12 BG966589
10	239.6	72.6	402	9 AI549800
11	239.2	72.5	327	10 BG148320
12	239.2	72.5	876	12 BI107286
13	238.6	72.3	735	12 BG967206
14	238.6	72.3	865	12 BI659552
15	238	72.1	420	9 AI120005
16	237.6	72.0	732	12 BG962768
17	235.4	71.3	806	12 BI108506
18	232.2	70.4	1063	10 BF577971
19	224.2	67.9	922	10 BF584560
20	216	65.5	974	10 BF577946
21	207	62.7	286	10 BG144775
22	201.6	61.1	339	9 AA710249
23	200.4	60.7	266	10 BG145361
24	199.4	60.4	344	13 BY214260
25	198.6	60.2	577	28 A2942606
26	175.4	53.2	671	11 AF240168
27	174.2	52.8	268	10 BG148476
28	171.2	51.9	756	28 BH054133
29	169.8	51.5	757	10 BG484518
30	164.4	49.8	465	9 AA404697
31	164.4	49.8	727	14 CB956193
32	163.8	49.6	798	10 BG426036
33	162.2	49.2	776	14 CB959429
34	161.2	48.8	755	14 CB957520
35	160.6	48.7	533	9 AM802126
36	160.6	48.7	717	14 CB957784
37	160.6	48.7	777	14 CB957974
38	160.6	48.7	779	14 CB986877
39	160.6	48.7	795	14 CB986276
40	160.6	48.7	889	14 CB985667
41	160.4	48.6	434	9 AA406486
42	160.2	48.5	808	14 CB984840
43	159.6	48.4	482	9 AV733856
44	159.6	48.4	519	9 AA405183
45	159.6	48.4	744	14 CB956406

## ALIGNMENTS

RESULT 1  
LOCUS BF137298  
DEFINITION 601781658F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4009670 5', mRNA sequence.  
ACCESSION BF137298  
VERSION BF137298.1 GI:10976338  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS 1 (bases 1 to 659)  
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-femail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM9246 row: c column: 15  
High quality sequence stop: 657.

FEATURES		Location/Qualifiers
	source	1..659 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:400670" /tissue_type="tumor, metastatic to mammary" /lab_host="DH10B" /clone_idb="NCI-CGAP_Lu30" /note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; transgenic model MN-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT		177 a 177 c 157 g 148 t
ORIGIN		
Query Match	75.9%; Score 250.4; DB 10; Length 659;	
Best Local Similarity	89.3%; Pred. No. 2e-63;	
MATCHES	293; Conservative 0; Mismatches 31; Indels 4; Gaps 2;	
Db	6 TGTGCTCACCAATTCCTCCAGCTTCTTGCGTGCCTCTAGGGACGAGGGCCACCATCTC	65
Db	42 TGTGCTGACCCAAATCTTAGCTTC-TTGGCTGTGTCTCTAGGGACGAGGGCCACCATT	100
Oy	66 CTGCAAGGCCAGCCAAAGTTGATTATGATGTGATAGTATATG--TTGTAACAACA	122
Db	101 CTGCAAGGCCAGCCAGATGTCTATTATAATGAATATGATATGACTGTTCCAA	160
Oy	123 GAACACGACGACGACCCAAATCTCTACCTATGTCTCATTCATCTAGAATCTGGAT	182
Db	161 GAACACGACGACGACCCAAATCTCTATATGCTGACATCCAACCTAATCTGGGGT	220
Oy	183 CCAAGCCAGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCATCTCT	242
Db	221 CCCTGCCAGTTTCACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCATCTCT	280
Oy	243 GGAGAGAGAGATGCTGCACACTTATTACTGTTCAGCTTTGTAATGAGATCTCTCCACGTT	302
Db	281 GGAGAGAGAGATGCTGCACACTTATTACTGTTCAGCAAGATATGAGATCTCTCCACGTT	340
Oy	303 CGGTCTGTGGACCAAGCTGAGCTGAAA 330	
Db	341 CGGTGTGGAGCACAAGCTGGAATCAA 368	
RESULT 2		
US	AW988429	407 bp mRNA linear EST 02-JUN-2000
US	ug08d07.y1 Soares_mammary_gland_MLNG Mus musculus cDNA clone	
INITIATION	IMAGE:1531021 5' similar to gb:X02484_rnal IG KAPPA CHAIN PRECURSOR	
V-IV REGION (HUMAN):	gb:M35669 Mouse Ig aberrantly rearranged	
ACCESSION	kappa-chain mRNA V-J2-C-region, (MOUSE), mRNA sequence.	
VERSION	AW988429	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 407) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT	Tumor Gene Index Unpublished Contact: Robert Strausberg, Ph.D. Email: cgepb@femail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:947121 Seq primer: -40RP from Gluco.	
FEATURES	Location/Qualifiers	

	source	1. .407	/organism="Mus musculus"
		/mol_type="mRNA"	
		/db_xref="taxon:10090"	
		/clone="IMAGE:1531021"	
		/sex="female (lactating)"	
		/tissue_type="mammary gland"	
		/lab_host="DH10B"	
		/clone_id="Soares_mammary_gland_NMLMG"	
		/note="Vector: pP7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pP7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT	100 a	104 c	106 g 97 t
ORIGIN			
Query Match	75.7%;	Score 249.8;	DB 10; Length 407;
Best Local Similarity	86.5%;	Pred. No. 2.2e-63;	
Matches 288;	Conservative 0;	Mismatches 42;	Indels 3; Gaps 1;
OY	1	GACATTGTGCTCACCAATTTCTCCAGCTTCCTTGCTGTCTCTAGGGCAGAGGGCCACC	60
Db	72	GACATTGTGCTGCCACCATCTCCAGCTTCCTTGCTGTCTCTAGGGCAGAGGGCCACC	131
OY	61	ATCTCCGCAGAAAGCGCCAGCAAGAAGTTGATTATGATGATGATATG--TGGTAC	117
Db	132	ATATCTCTGACAGCCAGCTGGAAGTTGATAGTTATGCACTAATTTATGACTGGTAC	191
OY	118	CACAGAAACAGAGACAGCCACCACCACTCTCCACCTATGCTGCATCCAATCTAGAAATCT	177
Db	192	CAGCAGAAACAGAGACAGCCACCACCAACTCTCTATGCTGCATCCAACCTAGAAATCT	251
OY	178	GGGATCCCAGCCAGGTTTAATGGCAGTGGGTCTGGACAGACTTCACCCCTACATCCAT	237
Db	252	GGGATCCCCTGACAGGTTCAATGGTGGTCTGGACAGACTTCACCCCTACATCCAT	311
OY	238	CCGTGGGAGGAGATGGCTGCACAACCTATTACTGTCAGAGCTTGTAAATGAGATCCGCC	297
Db	312	CCGTGGGAGGCTGATGATGTTTGACACCTATTACTGTCAGCAAAGTAAATGAGATCCGGT	371
OY	298	ACGTTCCGTGCTGGAGCCCAAGCTGGAGCTGAAA	330
Db	372	ACGTTCCGTGAGGAGCCCAAGCTGGAATCAA	404
RESULT 3			
AF240172/c			
LOCUS		683 bp	mRNA Linear HTC 30-APR-2001
DEFINITION			Mus musculus MRP9 mRNA, partial cds.
ACCESSION			AF240172
VERSION			AF240172.1 GI:13877293
KEYWORDS			HTC.
SOURCE			Mus musculus (house mouse)
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			1 (bases 1 to 683)
AUTHORS			Cui,D.-X., Zeng,G.-Y., Wang,F., Xu,J.R., Ren,D.O., Guo,Y.H., Tian,F.R., Yan,X.J., Hou,Y., Su,C.Z.
TITLE			Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice
JOURNAL			World J. Gastroenterol. 6 (5), 709-717 (2000)
PUBMED			11819679
REFERENCE			2 (bases 1 to 683)
AUTHORS			Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
TITLE			Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain
JOURNAL			Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80

REFERENCE	(2001)
AUTHORS	3 (bases 1 to 683)
TITLE	Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
JOURNAL	and Su,C. Direct Submission Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China
FEATURES	Location/Qualifiers
SOURCE	1..683
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="BALB/c"
	/db_xref="taxon:10090"
	/sex="male"
	/cell_type="intestinal gland cell"
	/note="derived from differential display PCR between irradiated mice with and without RNA injection"
	<1..352
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	/codon_start=2
	/product="MRP9"
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	/db_xref="GI:13877294"
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BASE COUNT	153 a 199 c 167 g 163 t 1 others
ORIGIN	
Query Match	74.2%; Score 245; DB 11; Length 683;
Best Local Similarity	85.6%; Pred. No. 8e-62;
Matches	285; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
OY	1 GACATTGGCTCACCACAATTCCTCCAGCTTCTTGCGCTGTCTCTAAGGCACAGGCCACC 60
DB	
	394 GACATCGTGTCCACCACTCTCCAGCTCTTTGGCTGTCTCTAAGGCACAGGCCACC 335
OY	61 ATCTCTGCAAGGCCAGCCAAAGTTGATTATGATGGTAGACTTATATG--TGGTAC 117
DB	
	334 ATCTCTGCAAGGCCAGCCAAAGTTGATTATGATGGTAGACTTATATGACTGGTTC 275
OY	118 CAACAGAAMCAGACAGCACGCCAACCAACTCTCATCTGATCGATCCAACTGAATCT 177
DB	
	274 CAGCAGAAAMCAGACAGCACGCCAACCAACTCTCATCTGATCGATCCAAACAGATCC 215
OY	178 GGGAATCCAGCAGAGTTAGTGGAGAGTGGGCTGGGACACACTTCACCCTCAATCAT 237
DB	
	214 GGGGTCCCTCCAGAGTTACTGTGGAGTGGGCTGGGACAGATTCACCTCAATCAT 155
OY	238 CCTGTGAGAGAGAGATGTGTCAACACATCTGATCGATCTTTTAATAGAGATCCGCC 297
DB	
	154 CCTATGAGAGAGATGTGTCAACACATCTGATCTTTTAATAGAGATCTTCCTTAC 95
OY	298 ACGTTCCGCTGGAGACCAAGCTGAGCTGAAA 330
DB	
	94 ACGTTCCGAGGGGAGCAACCAAGCTGAGCTGAAA 62
RESULT 4	
LOCUS	BG969221
DEFINITION	BG969221 1108 bp mRNA linear EST 12-JUN-2001
ACCESSION	602835202F1 NCI_CGAP_C024 Mus musculus cdna clone IMAGE:4989625 5'
VERSION	BG969221
KEYWORDS	Mus musculus (house mouse)
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ORGANISM	(bases 1 to 1108)

AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@rs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: L1AM11004 row: C column: 02 High quality sequence scop: 508.					
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	/lab_host="DH10B (TI phage-resistant)"					
	/clone_lib="NCI CGAP Co24"					
	/note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."					
BASE COUNT	286 a 417 c 244 g 161 t					
ORIGIN						
Query Match	74.2%; Score 245; DB 12; Length 1108;					
Best Local Similarity	93.5%; Pred. No. 1.le-61;					
Matches	289; Conservative 0; Mismatches 15; Indels 5; Gaps 3;					
OY	1	GACATTTGGCTCACCATTTCGCCAGCTCTTGCGTGTCCTAGAGGCGAGGCGCAC	60			
Db	63	GACATTTGGCTCACCATTTCGCCAGCTCTTGCGTGTCTTAGGCGAGGCGCGCAC	122			
OY	61	ATCTCTTGCAAGGCGCCAAAGTGTGATTATGATGTGATGATTATATG--TGGTAC	117			
Db	123	ATCTCTTGCAAGGCGCCAAAGTGTGATTATGATGTGATGATTATATG--TGGTAC	182			
OY	118	CAC-AGAACCCAGACAGCCCAACTCTCACCCTATGCTGATCATATAGAATC	176			
Db	183	CACATACAAACAGACAGCCCAACTCTCACCCTATGCTGATCATATAGAATC	242			
OY	177	TGGGATCCCACCAAGTTTAGTGCGAGGGGTGGGACAGACTTCACCCACACATCCA	236			
Db	243	TGGGATCCCACCAAGTTTAGTGCGAGGGGTGGGACAGACTTCACCCACACATCCA	302			
OY	237	TCTGTGTGAGAGAGATGCTGCAACCTATTACTGTCAGC-TTGTATAGAGATCCTC	295			
Db	303	CCCTGTGAGAGAGAGATGCTGCAACCTATTACTGTCAGCAGACAGTAATAGAGATCGT	362			
OY	296	CCACGTTTCG 304				
Db	363	ACACGTTTCG 371				
RESULT 5						
LOCUS	Bf581989	774 bp	mRNA	linear	EST 12-DEC-2000	
DEFINITION	60209944.F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4219426 5' ,					
ACCESSION	Bf581989					
VERSION	Bf581989.1 GI:11655610					
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1. (bases 1 to 774)					
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .					











TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LLM1108 row: 1 column: 22  
High quality sequence stop: 823.  
Location/Qualifiers

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/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="IMAGE:5039325"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
/stem\_cell\_origin=""  
/lab\_host="DH10B"  
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/note="Organ: Lung; Vector: pCMV-Sport6; Site: 1: Salt; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 239 a 242 c 192 g 203 t  
ORIGIN

Query Match 72.5%; Score 239.2; DB 12; Length 876;  
Best Local Similarity 85.8%; Pred. No. 4.9e-60;  
Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

OY 10 CTCACCATTCCTCCAGCTTCTTGCTGTCTCTAGGAGAGGCCACCATCTCCG 69  
DB 1 CTGACCCATCTCCAGCTTCTTGCTGTCTCTAGGAGAGGCCACCATCTCCG 60  
OY 70 AAGGACGACCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 126  
DB 61 AGAGCATGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 120  
OY 127 CCAGGACAGCCACCAACCTCTCAGTATGCTGATGATGATGATGATGATGATG 186  
DB 121 CCTGACAGCCACCAACCTCTCAGTATGCTGATGATGATGATGATGATGATG 180  
OY 187 GCCAGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
DB 181 GACAGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
OY 247 GAGGAGATGCTGCAACCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306  
DB 241 GCTGATGATGCTGCAACCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
OY 307 GCTGGGACCAAGCTGAGCTGAAA 330  
DB 301 TCGGGGACCAAGCTGAGCTGAAA 324

RESULT 13  
LOCUS BG967206 735 bp mRNA linear EST 12-JUN-2001  
DEFINITION 602833889F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:498086 5',  
mRNA sequence.  
ACCESSION BG967206  
VERSION BG967206.1 GI:14354843  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 735)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LLM1100 row: b column: 23  
High quality sequence stop: 730.  
Location/Qualifiers

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/organism="Mus musculus"  
/mol\_type="mRNA"  
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/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP\_Co24"  
/note="Organ: colon; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP library."

BASE COUNT 194 a 201 c 178 g 162 t  
ORIGIN

Query Match 72.3%; Score 238.6; DB 12; Length 735;  
Best Local Similarity 84.4%; Pred. No. 6.7e-60;  
Matches 281; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

OY 1 GACATTTGCTCCACCAATTCCTCAGCTTCTTGCTGTCTCTAGGAGAGGCCACC 60  
DB 86 GACATTTGCTCCACCAATTCCTCAGCTTCTTGCTGTCTCTAGGAGAGGCCACC 145  
OY 61 ATCTCTCTCAAGGCCCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 117  
DB 146 ATCTCTCTCAAGGCCCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 205  
OY 118 CAACGAAACCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 177  
DB 206 CAACGAAACCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 265  
OY 178 GGGATCCAGCAGGTTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 237  
DB 266 GGGATCCAGCAGGTTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 325  
OY 238 CCTGTGAGAGGAGGATGCTGCAACCTATCTGCTGCTGCTGCTGCTGCTGCTGCT 297  
DB 326 CCTGTGAGAGGAGGATGCTGCAACCTATCTGCTGCTGCTGCTGCTGCTGCTGCT 385  
OY 298 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330  
DB 386 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418

RESULT 14  
LOCUS B1659552 865 bp mRNA linear EST 12-SEP-2001  
DEFINITION 603303102F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:5340688 5',  
mRNA sequence.  
ACCESSION B1659552  
VERSION B1659552.1 GI:15573788  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 865)  
NIH-MGC <http://mgc.nci.nih.gov/>.





Db 302 CCTATGAGAGAGATGATTCTGCAATGTATTCTGTCAGCAAAAGTAAGGAGGTTCTTTGG 361  
Oy 298 ACGTTCGGTCTGGGACCAAGCTGGA 323  
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Db 362 ACGTTCGGTGGAGGACGAGCTGGA 387

Search completed: September 13, 2003, 06:41:26  
Job time : 2602 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 05:10:03 : Search time 64 Seconds  
(without alignments)  
2275.882 Million cell updates/sec

Title: US-09-759-112a-23  
Perfect score: 330  
Sequence: 1 gacattggtcaccattc.....ggaccaagctgagctgaa 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues  
al number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294.6	89.3	396	2	US-08-483-636-1 Sequence 1, Appl
2	294.6	89.3	396	2	US-08-483-632-1 Sequence 1, Appl
3	286.6	86.8	333	1	US-08-491-845-7 Sequence 7, Appl
4	283.4	85.9	393	3	US-08-579-378A-13 Sequence 13, Appl
5	262.6	79.6	393	1	US-08-137-117D-32 Sequence 32, Appl
6	262.6	79.6	393	1	US-08-436-717-32 Sequence 32, Appl
7	261	79.1	333	1	US-08-275-053-10 Sequence 10, Appl
8	261	79.1	333	1	US-08-275-053-16 Sequence 16, Appl
9	261	79.1	363	1	US-08-111-080-21 Sequence 21, Appl
10	261	79.1	363	1	US-08-111-080-21 Sequence 21, Appl
11	261	79.1	363	5	PCT-US93-07967-21 Sequence 21, Appl
12	257.8	78.1	339	2	US-08-553-497A-9 Sequence 9, Appl
13	257.8	78.1	363	1	US-08-111-080-17 Sequence 17, Appl
14	257.8	78.1	363	5	PCT-US92-07111-16 Sequence 16, Appl
15	257.8	78.1	363	5	PCT-US93-07967-17 Sequence 17, Appl
16	257.8	78.1	363	2	US-08-553-497A-5 Sequence 5, Appl
17	254.6	77.2	393	1	US-07-634-278-66 Sequence 66, Appl
18	249.8	75.7	393	1	US-08-477-728-66 Sequence 66, Appl
19	249.8	75.7	393	1	US-08-474-040-66 Sequence 66, Appl
20	249.8	75.7	393	1	US-08-487-200-66 Sequence 66, Appl
21	249.8	75.7	393	2	US-08-621-751A-9 Sequence 9, Appl
22	249.8	75.7	393	2	US-08-484-537-66 Sequence 66, Appl
23	249.8	75.7	393	2	US-08-553-497A-17 Sequence 17, Appl
24	246.2	74.6	717	2	US-08-656-906-24 Sequence 24, Appl
25	245	74.2	906	3	US-09-217-847-24 Sequence 3, Appl
26	245	74.2	906	3	US-08-442-542-3 Sequence 3, Appl
27	243.4	73.8	333	1	US-08-442-542-3 Sequence 3, Appl

28	243.4	73.8	333	3	US-08-765-469-3 Sequence 3, Appl
29	243.4	73.8	393	1	US-08-137-117D-24 Sequence 24, Appl
30	243.4	73.8	393	1	US-08-436-717-24 Sequence 24, Appl
31	243.4	73.8	1797	1	US-08-442-542-17 Sequence 17, Appl
32	243.4	73.8	1797	3	US-08-765-468-17 Sequence 17, Appl
33	242.4	73.5	783	4	US-08-487-283A-19 Sequence 19, Appl
34	239.4	72.5	333	1	US-08-207-169A-3 Sequence 3, Appl
35	238.6	72.3	336	3	US-09-065-059-14 Sequence 14, Appl
36	237	71.8	394	4	US-08-836-561-24 Sequence 24, Appl
37	237	71.8	394	4	US-09-434-122-24 Sequence 24, Appl
38	235.4	71.3	399	5	PCT-US94-14106-52 Sequence 52, Appl
39	235.4	71.3	428	3	US-08-589-939-4 Sequence 4, Appl
40	233.8	70.8	343	2	US-08-650-262-1 Sequence 1, Appl
41	233.8	70.8	723	5	PCT-US94-14106-56 Sequence 56, Appl
42	232.2	70.4	654	5	PCT-US96-13152-1 Sequence 1, Appl
43	231.4	70.1	332	3	US-08-881-037-58 Sequence 58, Appl
44	230.6	69.9	393	3	US-08-579-378A-17 Sequence 17, Appl
45	229	69.4	396	2	US-08-379-057-15 Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-08-483-636-1  
Sequence 1, Application US/08483636  
Patent No. 5914110  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESS: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483, 636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown









TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/111,080  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..363  
US-08-111-080-21

Query Match 79.1%; Score 261; DB 1; Length 363;  
Best Local Similarity 88.6%; Pred. No. 9,8e-80;  
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

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1 GACATTGGCTGCACCAATTCCTTGGCTGTCTCTAGGCGAGGCGCCACC 60  
61 ATCTCTGCAAGCGCCAGCCAAAGTGTGATATGATGATGATGATGATG- -TGTTAC 117  
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118 CAACGAAACACGAGCAGCAGCCCAAACTCTCCTACCTATGCTGATCCAACTAGAAATCT 177  
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238 CCGTGGAGGAGAGAGATGCTGCAACCTATTACTGCTGCTGATGATGATGATGATGATG- -TGTTAC 297  
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298 AGTTTCGGTGTGCTGGAGCAACCTGAGCTGAAA 330

301 ACCTTCGGTGTGCTGGAGCAACCTGAGCTGAAA 333

RESULT 10  
US-08-211-980-21  
Sequence 21, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Onno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..363  
US-08-211-980-21

Query Match 79.1%; Score 261; DB 1; Length 363;  
Best Local Similarity 88.6%; Pred. No. 9,8e-80;  
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

1 GACATTGGCTGCACCAATTCCTTGGCTGTCTCTAGGCGAGGCGCCACC 60  
1 GACATTGGCTGCACCAATTCCTTGGCTGTCTCTAGGCGAGGCGCCACC 60  
61 ATCTCTGCAAGCGCCAGCCAAAGTGTGATATGATGATGATGATGATG- -TGTTAC 117  
61 ATCTCTGCAAGCGCCAGCCAAAGTGTGATATGATGATGATGATGATG- -TGTTAC 117  
61 ATCTCTGCAAGCGCCAGCCAAAGTGTGATATGATGATGATGATGATG- -TGTTAC 120  
118 CAACGAAACACGAGCAGCAGCCCAAACTCTCCTACCTATGCTGATCCAACTAGAAATCT 177  
118 CAACGAAACACGAGCAGCAGCCCAAACTCTCCTACCTATGCTGATCCAACTAGAAATCT 177  
121 GAGCGAAACACGAGCAGCAGCCCAAACTCTCCTACCTATGCTGATCCAACTAGAAATCT 180  
121 GAGCGAAACACGAGCAGCAGCCCAAACTCTCCTACCTATGCTGATCCAACTAGAAATCT 180  
178 GGGATCCAGCAGGCTTAAAGTGGAGTGGCTGTGGAGACAGACTTACCCCTCAACATCAT 237  
178 GGGATCCAGCAGGCTTAAAGTGGAGTGGCTGTGGAGACAGACTTACCCCTCAACATCAT 237



Db	181	GGGGTCCCTGACAGGTTTCAGTGGCGTGGGGTCTGAGACAGCTTCACCCCTACCATTTGAT	240
Qy	238	CCGTGGAGAGGAGGAGATGCTGCACACCTATTACTGTGTCAGCTTTAATGAGAGATCCGCC	297
Db	241	CCGTGGAGAGCGATGATGATGCTGCACACCTATTACTGTGACCAATAATGAGATCCGCTC	300
Qy	298	ACGTTGCGTGTGGGACCAAGCTGAGCTGAATA	330
Db	301	ACGTTGCGTGTGGGACCAAGCTGAGCTGGAATA	333

RESULT 11  
PCT-US93-07967-21

APPLICANT: Ohno, Tsuneva  
 TITLE OF INVENTION: HIV Immunotherapeutics  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ADDRESSEE: Borun  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 City: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/07967  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/07111  
 FILING DATE: 24-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/039,457  
 FILING DATE: 22-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 REFERENCE/DOCKET NUMBER: 3129  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 363 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1...363  
 PCT-US93-07967-21

Query Match	79.18;	Score 261;	DB 5;	Length 363;
Best Local Similarity	88.68;	Pred. No. 9.8e-80;		
Matches 295; Conservative	0;	Mismatches 35;	Indels 3;	Gaps 1;

Qy	GACATGTGTGTCACCAATTTCTCCAGTTDTTTGGCTGTGTCTCAGGCAAGAGGGCCACC	60
Db	GACATGTGTGTCACCAATCTCCAGTTCTTTGGCTGTGTCTCTAGGGCAAGAGGGCCACC	60
Qy	ATCTCTCGCAAGCCAGCCAAAGTGTTCATTATGCATGTGTATAGTTATATG---TGTATC	117
Db	ATATCTCGCAAGCCAGTGAAGTGTGTGTAATTATTTGGCAATAGCTTTATCCACTGTATC	120

QY	110	CAACACAAACCGAGGACAGCCACCCAAACCTCCACCTATGGTCGATCAACTATGAACTC	177
Db	121	CACACAAACCGAGGACAGTCACCCAACTCCCTCATCTATGTTTGATCAACCTTGAATCT	180
QY	178	GGGATCCACGACGAGTTTATGTCGACAGTGGGTCGTGGGACAGACTTCACCCCTCAACATCAT	237
Db	181	GGGGTCCCTCCGACGGTTCAGTGGGACGTGGGTCGTAGGACAGACTTCACCCCTCACATTCAT	240
QY	238	CCTGTGGAGGAGAGGATGCTGCACACTATTACTGTCACTTTGTTAATGAGATCCTCC	297
Db	241	CCGTGTGAAGCTGATGATGCTGCACCACTATTACTGTCAAGCAAAATATGAGGATCCGCTC	300
QY	298	ACGTTGGTGTGGGACCAAGCTGGAGCTGAAA	330
Db	301	ACGTTGGTGTGGGACCAAGCTGGAGCTGAAA	333

RESULT 12  
US-08-553-497A-9  
; Sequence 9, Application US/08553497A  
; Patent No. 5844093

APPLICANT: KETTLEBOROUGH, C. A.  
 APPLICANT: BENDIG, MARY M.  
 APPLICANT: ANSELL, KEITH H.  
 APPLICANT: GUSSON, DETLEF  
 APPLICANT: ADAN, JAUME  
 APPLICANT: MITJANS, FRANCESC  
 APPLICANT: ROSELL, ELISABET  
 APPLICANT: BLASCO, FRANCESC  
 APPLICANT: PILATS, JAUME  
 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.  
 STREET: 2200 CLARENDON BLVD. SUITE 1400  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: US  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/553,497A  
 FILING DATE: 17-NOV-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/EP95/00978  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 94104160.0  
 FILING DATE: 17-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 94118970.6  
 FILING DATE: 02-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAMLET-KING, DIANA  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: MERCK 1726  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333  
 TELEFAX: 703-243-6410  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 339 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

? HYPOTHETICAL: NO  
 ? ANTI-SENSE: NO  
 ? FRAGMENT TYPE: N-terminal  
 ? ORIGINAL SOURCE:  
 ? ORGANISM: mouse  
 ? STRAIN: Balb/c  
 ? DEVELOPMENTAL STAGE: adult  
 ? TISSUE TYPE: lymph node  
 ? IMMEDIATE SOURCE:  
 ? CLONE: L3 11d (light chain)  
 ? FEATURE:  
 ? NAME/KEY: CDS  
 ? LOCATION: 1..339  
 ? US-08-553-497A-9

Query Match 78.1%; Score 257.8; DB 2; Length 339;  
 Best Local Similarity 88.0%; Pred. No. 1.2e-78;  
 Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

1 GACATTGTCCTCACCATTCTCCAGCTTCTTGCTGTGTCTCTAGAGGAGGCGCACC 60  
 1 GACATTGACCTCACCAGCTCAGCTTCTTGCTGTGTCTCTAGAGGAGGCGCACC 60  
 61 ATCTCTGCAAGCCAGCCCAAGTGTATATGATGTGATGATTATATG---TGTAC 117  
 61 ATCTCTGCAAGCCAGCCCAAGTGTATATGATGTGATGATTATATG---TGTAC 117  
 118 CAACAGAAACGAGAGAGAGCCCAACACTCTCAGTATGCTGATCAGCTAGAGTCT 177  
 121 CACAGAAACGAGAGAGAGCCCAACACTCTCAGTATGCTGATCAGCTAGAGTCT 180  
 178 GGGATCCAGCAGGTTTATGTCAGTGTGCTGTGGACAGACTTCACTCAACATCAT 237  
 181 GGGATCCAGCAGGTTTATGTCAGTGTGCTGTGGACAGACTTCACTCAACATCAT 240  
 238 CCTGTGAGAGAGAGAGTCTCAGCTTCTCTAGCTTCTGTAATAGAGATCTCTCC 297  
 241 CCTGTGAGAGAGAGTCTCAGCTTCTCTAGCTTCTGTAATAGAGATCTCTCC 300  
 298 ACCTTGGGTGCTGGAGCAGCAAGCTGGAGCTGAAA 330  
 301 ACCTTGGGTGCTGGAGCAGCAAGCTGGAGCTGAAA 333

RESULT 13  
 US-08-111-080-17  
 Sequence 17, Application 08/111080  
 Patent No. 555865  
 GENERAL INFORMATION:

APPLICANT: Onno, Tsuneya  
 TITLE OF INVENTION: HIV Immunotherapeutics  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/111,080  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/748,562  
 FILING DATE: 22-AUG-1991  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/07111  
 FILING DATE: 24-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/039,457  
 FILING DATE: 22-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 REFERENCE/DOCKET NUMBER: 31629  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ. ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 363 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..363  
 US-08-111-080-17

Query Match 78.1%; Score 257.8; DB 1; Length 363;  
 Best Local Similarity 88.0%; Pred. No. 1.2e-78;  
 Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

1 GACATTGTCCTCACCATTCTCCAGCTTCTTGCTGTGTCTCTAGAGGAGGCGCACC 60  
 1 GACATTGTCCTCACCATTCTCCAGCTTCTTGCTGTGTCTCTAGAGGAGGCGCACC 60  
 61 ATCTCTGCAAGCCAGCCCAAGTGTATATGATGTGATGATTATATG---TGTAC 117  
 61 ATCTCTGCAAGCCAGCCCAAGTGTATATGATGTGATGATTATATG---TGTAC 117  
 118 CAACAGAAACGAGAGAGAGCCCAACACTCTCAGTATGCTGATCAGCTAGAGTCT 177  
 121 CACAGAAACGAGAGAGAGCCCAACACTCTCAGTATGCTGATCAGCTAGAGTCT 180  
 178 GGGATCCAGCAGGTTTATGTCAGTGTGCTGTGGACAGACTTCACTCAACATCAT 237  
 181 GGGATCCAGCAGGTTTATGTCAGTGTGCTGTGGACAGACTTCACTCAACATCAT 240  
 238 CCTGTGAGAGAGAGAGTCTCAGCTTCTCTAGCTTCTGTAATAGAGATCTCTCC 297  
 241 CCTGTGAGAGAGTCTCAGCTTCTCTAGCTTCTGTAATAGAGATCTCTCC 300  
 298 ACCTTGGGTGCTGGAGCAGCAAGCTGGAGCTGAAA 330  
 301 GCGTTCGCTAGTGGAGCAGCAAGCTGGAGCTGAAA 333

RESULT 14  
 US-08-211-980-17  
 Sequence 17, Application US/08211980  
 Patent No. 566569  
 GENERAL INFORMATION:

APPLICANT: Onno, Tsuneya  
 TITLE OF INVENTION: HIV Immunotherapeutics  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
US-08-211-980-17

Query Match      78.1%; Score 257.8; DB 1; Length 363;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
```

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QY 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
DB 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
QY 61 ATCTCTGCAAGGCGCAAGGTGATTTATGATGATGATGATGATGATGATG 117
DB 61 ATCTCTGCAAGGCGCAAGGTGATTTATGATGATGATGATGATGATGATG 117
QY 118 CAACGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177
DB 121 CAGCAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 178 GGGATCCAGCAGGCTTTAGTGGCAGTGGGCTCTGGGACAGACTTCAACAT 237
DB 181 GGGGTCCTGCGCAGGCTTACAGTGGGCTCTAGGACAGACTTCAACAT 240
QY 238 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
DB 241 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 298 ACCTTCGCTGCTGGAGCAGCTGAGCTGAAA 330
DB 301 GCGTTCGCTACTGGAGCAGCTGAGCTGAAA 333
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RESULT 15
PCT-US92-07111-16
Sequence 16, Application PC/TUS9207111
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
Street
```

```
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 19920824
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
PCT-US92-07111-16
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Query Match      78.1%; Score 257.8; DB 5; Length 363;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
```

```
QY 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
DB 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
QY 61 ATCTCTGCAAGGCGCAAGGTGATTTATGATGATGATGATGATGATGATG 117
DB 61 ATCTCTGCAAGGCGCAAGGTGATTTATGATGATGATGATGATGATGATG 117
QY 118 CAACGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177
DB 121 CAGCAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 178 GGGATCCAGCAGGCTTTAGTGGCAGTGGGCTCTGGGACAGACTTCAACAT 237
DB 181 GGGGTCCTGCGCAGGCTTACAGTGGGCTCTAGGACAGACTTCAACAT 240
QY 238 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
DB 241 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 298 ACCTTCGCTGCTGGAGCAGCTGAGCTGAAA 330
DB 301 GCGTTCGCTACTGGAGCAGCTGAGCTGAAA 333
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Search completed: September 13, 2003, 06:42:41  
Job time : 67 secs

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OY 298 ACGTTCGGTGTGGAGCAAGCTGGAGCTGAAA 330  
 |||||  
 DB 361 ACGTTCGGTGTGGAGCAAGCTGGAGAAATCAAA 393

## RESULT 4

US-10-216-484-10  
 ; Sequence 10, Application US/10216484  
 ; Publication No. US20030103976A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa  
 ; APPLICANT: Haruyama, Hideyuki  
 ; APPLICANT: Nakahara, Kaori  
 ; APPLICANT: Takahashi, Ikuko  
 ; APPLICANT: Takahashi, Tomru  
 ; TITLE OF INVENTION: Anti-Fas Antibodies  
 ; FILE REFERENCE: 980126CIP/Hg  
 ; CURRENT APPLICATION NUMBER: US/10/216,484  
 ; CURRENT FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US/09/499,662  
 ; PRIOR FILING DATE: 2000-02-09  
 ; PRIOR APPLICATION NUMBER: US 09/053,583  
 ; PRIOR FILING DATE: 1998-04-01  
 ; NUMBER OF SEQ ID NOS: 165  
 ; SEQ ID NO 10  
 ; LENGTH: 714  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(714)  
 ; FEATURE:  
 ; NAME/KEY: mat peptide  
 ; LOCATION: (61)..(714)  
 ; FEATURE:  
 ; NAME/KEY: sig peptide  
 ; LOCATION: (1)..(60)  
 US-10-216-484-10

Query Match Best Local Similarity 94.6%; Score 293; DB 14; Length 714;  
 Pred. No. 2,6e-91;

Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

OY 1 GACATTTGCTCCACCAATTTCTCCAGCTTTGGCTGTCTCTAGGAGGAGGCGCACC 60  
 |||||  
 DB 61 GACATTTGCTCCACCAATTTCTCCAGCTTTGGCTGTCTCTAGGAGGAGGCGCACC 120  
 |||||  
 61 ATCTCTGTCAGAGCCAGCCAAAGTGTGATTTAGATGTGATAGTTATATG--TGGTAC 117  
 |||||  
 121 ATCTCTGTCAGAGCCAGCCAAAGTGTGATTTAGATGTGATAGTTATATGAACTGGTAC 180  
 |||||  
 OY 118 CAACAGAAACGAGAGAGGAGCCACCAACCTCCTACCTATAGCTGCATCTAGANATCT 177  
 |||||  
 DB 181 CAACAGAAACGAGAGAGGAGCCACCAACCTCCTATAGCTGCATCTAGANATCT 240  
 |||||  
 OY 178 GGGATCCAGAGGAGGTTTATAGTGGAGTGGCTGTGGAGAGAGCTTCAACCTCAACATCAT 237  
 |||||  
 DB 241 GGGATCCAGAGGAGGTTTATAGTGGAGTGGCTGTGGAGAGAGCTTCAACCTCAACATCAT 300  
 |||||  
 OY 238 CCTGTGAGAGAGAGAGATGCTGCAACCTATTTACTGTCACTTTGTAATGAGAGATCCTCC 297  
 |||||  
 DB 301 CCTGTGAGAGAGAGAGATGCTGCAACCTATTTACTGTCAACCAAGTAATAGAGATCCTCGG 360  
 |||||  
 OY 298 ACGTTCGGTGTGGAGCAAGCTGGAGCTGAAA 330  
 |||||  
 DB 361 ACGTTCGGTGTGGAGCAAGCTGGAGAAATCAAA 393

RESULT 5  
 US-09-903-327A-3  
 ; Sequence 3, Application US/09903327A  
 ; Patent No. US2002016433A1  
 ; GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.  
 APPLICANT: Li, Erluang  
 TITLE OF INVENTION: FUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR  
 TITLE OF INVENTION: GENE  
 FILE REFERENCE: 22908-1228  
 CURRENT APPLICATION NUMBER: US/09/903,327A  
 CURRENT FILING DATE: 2001-07-10  
 PRIOR APPLICATION NUMBER: 09/613,017  
 PRIOR FILING DATE: 2000-07-10  
 NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 831  
 ; TYPE: DNA  
 ; ORGANISM: Mouse  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (13)..(726)  
 ; OTHER INFORMATION: DAY-1 light chain, penton base monoclonal antibody  
 US-09-903-327A-3

Query Match Best Local Similarity 86.8%; Score 286.6; DB 10; Length 831;  
 Pred. No. 4.7e-89;

Matches 311; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

OY 1 GACATTTGCTCCACCAATTTCTCCAGCTTTGGCTGTCTCTAGGAGGAGGCGCACC 60  
 |||||  
 DB 73 GACATTTGCTCCACCAATTTCTCCAGCTTTGGCTGTCTCTAGGAGGAGGCGCACC 132  
 |||||  
 OY 61 ATCTCTGTCAGAGCCAGCCAAAGTGTGATTTAGATGTGATAGTTATATG--TGGTAC 117  
 |||||  
 DB 133 ATCTCTGTCAGAGCCAGCCAAAGTGTGATTTAGATGTGATAGTTATATGAACTGGTAC 192  
 |||||  
 OY 118 CAACAGAAACGAGAGAGGAGCCACCAACCTCCTACCTATAGCTGCATCTAGANATCT 177  
 |||||  
 DB 193 CAACAGAAACGAGAGAGGAGCCACCAACCTCCTATAGCTGCATCTAGANATCT 252  
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 OY 178 GGGATCCAGAGGAGGTTTATAGTGGAGTGGCTGTGGAGAGAGCTTCAACCTCAACATCAT 237  
 |||||  
 DB 253 GGGATCCAGAGGAGGTTTATAGTGGAGTGGCTGTGGAGAGAGCTTCAACCTCAACATCAT 312  
 |||||  
 OY 238 CCTGTGAGAGAGAGAGATGCTGCAACCTATTTACTGTCACTTTGTAATGAGAGATCCTCC 297  
 |||||  
 DB 313 CCTGTGAGAGAGAGAGATGCTGCAACCTATTTACTGTCAACCAAGTAATAGAGATCCTCGG 372  
 |||||  
 OY 298 ACGTTCGGTGTGGAGCAAGCTGGAGCTGAAA 330  
 |||||  
 DB 373 ACGTTCGGTGTGGAGCAAGCTGGAGAAATCAAA 405

RESULT 6  
 US-10-216-484-53  
 ; Sequence 53, Application US/10216484  
 ; Publication No. US20030103976A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa  
 ; APPLICANT: Haruyama, Hideyuki  
 ; APPLICANT: Nakahara, Kaori  
 ; APPLICANT: Takahashi, Ikuko  
 ; APPLICANT: Takahashi, Tomru  
 ; TITLE OF INVENTION: Anti-Fas Antibodies  
 ; FILE REFERENCE: 980126CIP/Hg  
 ; CURRENT APPLICATION NUMBER: US/10/216,484  
 ; CURRENT FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US/09/499,662  
 ; PRIOR FILING DATE: 2000-02-09  
 ; PRIOR APPLICATION NUMBER: US 09/053,583  
 ; PRIOR FILING DATE: 1998-04-01  
 ; NUMBER OF SEQ ID NOS: 165  
 ; SEQ ID NO 53  
 ; LENGTH: 768  
 ; TYPE: DNA









Query Match	77.28	Score 254.6	DB 14	Length 768
Best Local Similarity	87.48	Pred. No. 6e-78		
Matches 291; Conservative	0	Mismatches 39;	Indels 3;	Gaps 1;

Qy	1	GACATGTGCTCACCAATTCCTCACCTTCCTTGGCTGTGTCTCTAGGGACAGAGGGCCACC	60
Db	100	GACATGTGCTCACCAATTCCTCACCTTCCTTGTCTGTCTCCAGGGAGAGGGCCACC	159
Qy	61	ATCTCCTCGAAGCCACGCCAAAGTTGTGATTATGATGGTATGATATATG--TGGTAC	117
Db	160	CTCTCTGGAAAGGCCACGCCAAAGTTGATTATGATGATGGTATGATTATGAACTGGTAC	219
Qy	118	CACACAGAAACACAGACAGCCACCCAACTCCCTCACCCTTGGTGCATCCAACTAGATCT	177
Db	220	CACACAGAAACACAGACAGGCCACCACGACTCCCTCATCTATGCTGATCCATCTCGAATCT	279
Qy	178	GGGATCCACGACGGTTTAGTGGCAGTGGGCTGGGACACACTTCACCCCTCAACATTCAT	237
Db	280	GGGATCCACGACAGGTTTAGTGGCAGTGGGCTGGGACAGACTTCACCCCTCACATCTCT	339
Qy	238	CCGTGTGAGAGAGAGAGATGCTCAACACTTACTGTCAAGTTGTATATGAGAGATCTCCC	297
Db	340	CGTCTGGAGCCGCGGATTTTGCACATCTATTAAGTGTACGACAAATATATGAGATCTCGG	399
Qy	298	ACGTTGGGTCTGGAGCCAAAGCTGGAAGCTGAAA	330
Db	400	ACGTTGGGTCTAAGGCCACGAGCTGGAATAATCAAA	432

RESULT 14  
US-10-171-452A-37  
; sequence 37, Application US/10171452A

1 APPLICANT: Frewin, Mark  
 2 APPLICANT: Maldmann, Herman  
 3 APPLICANT: Gorman, Scott  
 4 APPLICANT: Hale, Geoff  
 5 APPLICANT: Rao, Patricia  
 6 APPLICANT: Kornaga, Tadeusz  
 7 APPLICANT: Ringler, Douglas  
 8 APPLICANT: Cobbold, Stephen  
 9 APPLICANT: Winsor-Hines, Dawn  
 10 TITLE OF INVENTION: Trx1 Antibody and Uses Therefor  
 11 FILE REFERENCE: 695458-59

```

? CURRENT APPLICATION NUMBER: US10/171,452A
? CURRENT FILING DATE: 2003-02-10
? PRIOR APPLICATION NUMBER: US60/373,471
? PRIOR FILING DATE: 2002-04-18
? PRIOR APPLICATION NUMBER: US60/373,470
? PRIOR FILING DATE: 2002-04-18
? PRIOR APPLICATION NUMBER: US60/345,194
? PRIOR FILING DATE: 2002-10-19
? PRIOR APPLICATION NUMBER: GB0122724.8
? PRIOR FILING DATE: 2001-09-20
? PRIOR APPLICATION NUMBER: GB0114517.6
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 60
? SEQ ID NO 37
? LENGTH: 717
? TYPE: DNA
? ORGANISM: Artificial
? FEATURE:
? OTHER INFORMATION: DNA Sequence encoding light chain of humanized antibody
? US-10-171-452A-37

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Query Match	76.7%	Score 253;	DB 14;	length 717;
Best Local Similarity	-87.1%;	Pred. NO. 2.1e-77;		
Matches 290; Conservative	0;	Mismatches 40;	Indels 3;	Gaps 1

QY	1	GAAATTGTCTCAACCAAAATTCCTCAGCTCTTTGGCTGTGTCTTAAAGGCAAGGGCCACC	60
Db	61	GCAATTGTATATACCCAATCTCCAAATTCCTTGGCTGTCTCTTAAGTGAAGAGGCCACC	120
QY	61	ATCTCCTGCAGAGCCACGCCAAAGTGTGATTATGATGTGATAGTTAATG--TGTATC	117
Db	121	ATCAATCTGAAGAGCCACGCCAAAGTGTGATTATGATGTGATAGTTAATGCAACTGCTAT	180
QY	118	CACAGCAAAACAGAGAGCCACCCAAATCCTCAGCTTATGCTGATCCATCAATCTGAAATCT	177
Db	181	CACACAAAAACAGAGAGCCACCCAAATCCTCAGCTTATGCTGATCCATCAATCTGAAATCT	240
QY	178	GGGATCCCAAGCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCAAT	237
Db	241	GGGGTCCCAAGAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCAAT	300
QY	238	CCGTGTGAGAGAGAGATCTGCACACCTAATTAAGTCTAGCTTTGTAATGATGAAGCTCCCC	297
Db	301	TCCTCTCAGAGCGAGATGTTGCACTATTAATTAAGTCTAGCAAGAGCTTTCAGAGACCCTCG	360
QY	298	ACGTTGGTGTCTGGAGCCAAAGCTGAGCTGA	330
Db	361	ACGTTGGTGTGAGAGTACCAAGGTCGCAAAATTC	393

RESULT 15  
US-10-171-452A-43

; Sequence 43, Application US/10171452A

; GENERAL INFORMATION:

APPLICANT: Frewin, Mark

APPLICANT: Gorman, Scott

APPLICANT: Rao, Patricia

APPLICANT: kornaga, Tadeusz

APPLICANT: Cobbold, Stephen

TITLE OF INVENTION: TRX1 Ant

FILE REFERENCE: 695458-59  
CURRENT APPLICATION NUMBER: IIS/10/171-452A

CURRENT FILING DATE: 2003-02-10

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US60/345,194



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 04:56:01; Search time 2855 Seconds

(without alignments)  
4728.608 Million cell updates/sec

Title: US-09-759-112a-23

Perfect score: 330

Sequence: 1 gacatgagctaccacattc.....ggaccaagctgagctgaa 330

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

al number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb\_om: \*  
5: gb\_ov: \*  
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7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_pro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
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14: gb\_vl: \*  
15: em\_ba: \*  
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34: em\_htg\_pin: \*  
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36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
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39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293	88.8	333	6 E30643	E30643 Antibody an
2	293	88.8	363	6 MUSL2021CK	M97869 Mouse hybr
3	293	88.8	714	6 BD090542	BD090542 Drug cont
4	293	88.8	714	6 BD090651	BD090651 Drug cont
5	293	88.8	714	6 E40005	E40005 Drug contal
6	293	88.8	714	6 E40813	E40813 Humanized a
7	293	88.8	714	6 E43359	E43359 Humanized a
8	293	88.8	877	6 E31225	E31225 Device for
9	293	88.8	925	6 E30616	E30616 Antibody an
10	293	88.8	925	6 E30617	E30617 Antibody an
11	289.8	87.8	354	10 MUSL71IGKV	M97875 Mouse hybr
12	289.8	87.8	363	10 MUSL931GKV	M97879 Mouse hybr
13	289.8	87.8	393	10 AF045518	AF045518 Mus muscu
14	288.2	87.3	333	6 E07408	E07408 cDNA encodi
15	288.2	87.3	333	6 MMA005355	AJ005355 Mus muscu
16	288.2	87.3	363	10 MUSL34IGKV	M97871 Mouse hybr
17	286.6	86.8	333	6 AR014069	AR014069 Sequence
18	286.6	86.8	333	6 S54207	S54207 V kappa 21-
19	286.6	86.8	831	6 AX392999	AX392999 Sequence
20	286.2	86.7	350	10 MUSIGKABBC	M92401 Mouse Ig Ka
21	285	86.4	333	10 MUSIGLSB	M80406 Mouse Igl c
22	285	86.4	333	10 S42888	S42888 Ig V kappa
23	285	86.4	334	6 E02169	E02169 DNA encodin
24	285	86.4	336	10 NMIGLC310	X65091 M.musculus
25	285	86.4	336	10 NMIGLC404	X65092 M.musculus
26	285	86.4	393	10 S50265	S50265 Ig VL-antl-
27	285	86.4	396	10 AF207705	AF207705 Mus muscu
28	285	86.4	744	12 AF402256	AF402256 Synthetic
29	283.6	85.9	333	10 AY173024	AY173024 Mus muscu
30	283.4	85.9	333	10 AF112403	AF112403 Mus muscu
31	283.4	85.9	333	10 AF321952	AF321952 Mus muscu
32	283.4	85.9	336	10 MUSIGKAAW	M31962 Mouse Ig re
33	283.4	85.9	393	6 AR144017	AR144017 Sequence
34	281.8	85.4	336	10 MM0012372	AJ012372 Mus muscu
35	280.8	85.1	360	10 MUSIGKAF	M61046 Mus musculu
36	280.8	85.1	900	6 I08223	I08223 Sequence 1
37	277.6	84.1	351	10 MUSIGKABH	M92406 Mouse Ig ka
38	276	83.6	333	10 MMVLE10	X51854 Mouse mRNA
39	276	83.6	353	10 MUSIGKABD	M92402 Mouse Ig ka
40	275.4	83.5	336	10 NMIGLC413	X65093 M.musculus
41	275.4	83.5	768	6 BD090559	BD090559 Drug cont
42	275.4	83.5	768	6 BD090668	BD090668 Drug cont
43	275.4	83.5	768	6 E40022	E40022 Drug contal
44	275.4	83.5	768	6 E40830	E40830 Humanized a
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## ALIGNMENTS

RESULT 1  
LOCUS E30643 333 bp DNA linear PAT 18-JUN-2001  
DEFINITION Antibody and nucleic acid encoding the same.  
ACCESSION E30643.1 GI:13017209  
VERSION E30643.1  
KEYWORDS JP 1999332563-A/30.  
SOURCE Mus sp.  
ORGANISM Mus sp.

REFERENCE  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE 1 (bases 1 to 333)  
JOURNAL Mitsuhashi, O., Takayuki, K. and Ikuno, M.  
Antibody and nucleic acid encoding the same  
Patent: JP 1999332563-A 30 07-DEC-1999;

Pred. No. is the number of results predicted by chance to have a

COMMENT	OS	Mus sp. (mouse)	JP 1999332563-A/30
PD	07-DEC-1999		
PF	26-MAY-1998	JP 1998165034	
PR			
PI	MITSUHARU ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO		
PC	C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08		
PC	C12N15/00,		
PC	C12N15/00,		
CC	Strandedness: Double;		
CC	Topology: Linear;		
FT	key	1.333	
FT	source	/organism='Mus sp. (mouse)'	
FEATURES	source	1.333	
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Query Match	88.8%; Score 293; DB 6; Length 333;		
Best Local Similarity	4.6%; Pred. No. 1, le-88;		
Matches	315; Conservative 0; Mismatches 15; Indels 3; Gaps 1		
OY	1 GACATTGCTCACCATTCTCCACCTCTTTGGCTGTCTCTAGGCGAGGGCCACC	60	
DB	1 GACATTGCTCACCATTCTCCACCTCTTTGGCTGTCTCTAGGCGAGGGCCACC	60	
OY	61 ATCTCTCTGAGGCGCCAGCCCAAGTGTATATATGATGTGATAGTATATG--TGTCAC	117	
DB	61 ATCTCTCTGAGGCGCCAGCCCAAGTGTATATGATGTGATAGTATATG--TGTCAC	120	
OY	118 CACAGAAACACGAGCAGCAGCCCAACCTCCACCTAGTGCATGCATCTAGATCT	177	
DB	121 CACAGAAACACGAGCAGCAGCCCAACCTCCACCTAGTGCATGCATCTAGATCT	180	
OY	178 GGGATCCGAGCAGGATTTAGTGGCAGTGGCTCTGGAGACAGATCCCTCAACATCCAT	237	
DB	181 GGGATCCGAGCAGGATTTAGTGGCAGTGGCTCTGGAGACAGATCCCTCAACATCCAT	240	
OY	238 CCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTCAAGCTTTGTAATGAGGATCTCC	297	
DB	241 CCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTCAAGCAAGTAGGAGATCTCCG	300	
OY	298 ACCTTGGCTGCTGGAGCCACGACCTGGAGCTGAAC	330	
DB	301 ACCTTGGCTGCTGGAGCCACGACCTGGAGCTGAAC	333	
RESULT 2	MUSL202IGK	363 bp	linear
DEFINITION	Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial cds.		
ACCESSION	M97869		
VERSION	M97869.1		
KEYWORDS	V-region; Immunoglobulin light chain; Immunoglobulin-kappa; processed gene.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 363)		
TITLE	Lothman,K.L., Buck,D.W., Garrillo,M.A. and Kennedy,R.C.		
JOURNAL	Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence		
COMMENT	Unpublished (1992)		
FEATURES	Original source: text: Mus musculus (strain BALB/c, sub-species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.		
Location/Qualifiers			

	source	1. .363 /organism="Mus musculus" /mol_type="mRNA" /strain="BALB/c" /sub_species="domesticus" /db_xref="taxon:10090" /map=6" /tissue_type="SP20-BALB/c fusion hybridoma" 1. .363 /gene="Irk" (1.11) : .363 /gene="Irk" /standard_name="L202; monoclonal antibody (CD4 antigen specificity)"
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	gene	
	BASE COUNT	93 a 96 c 92 g 82 t
	ORIGIN	
	Query Match	88.8%; Score 293; DB 10; Length 363;
	Best Local Similarity	94.6%; Pred. No. 1.1e-88;
	Matches 315; Conservative	0; Mismatches 15; Indels 3; Gaps 1
OY	1	GACATTGTGCTCACCATTCTCCAGCTTCTTTGGCTGTGTCTCTATGGAGCGAGGGCCACC 60
Dd	1	GACATTGTGCTGACCCCAATCTCCACTCTTGCGTGTGTCTCTATGGAGCGAGGGCCACC 60
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Dd	61	ATTCCTCTCAAGGCCAGCCAAAGTTGTATTATGATGGTAGATTATAATGAACATGGTATC 120
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Dd	121	CACACGAAGAACAAGGACGACGCCAACCCCTCATCTATGTGCATCATCTAGAAATCT 180
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Dd	181	GGGATCCAGCACGAGTTTGTGTGGCAGTGGTCTGTGGAGACAGACTTACCCCTCAACATCAT 240
OY	238	CCTGTGAGAGGAGAGATGCTGCACACTTAATCTCATGCTTTGTAATGAGATCTCTCCC 297
Dd	241	CCTGTGAGAGGAGAGATGCTGCACACTTAATCTCATGAGTAATACGATCTCTCCCC 300
OY	298	ACGTTGGTGGTGGGACCAAGCTGGAGCGTAAA 330
Dd	301	ACGTTGGGAGGGGGACCAAGCTGGAGATATAA 333
RESULT 3		
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LOCUS	BD090542	714 bp DNA linear PAT 27-AUG-2001
DEFINITION	Drug containing humanized anti-Fas antibody.	
ACCESSION	BD090542	
VERSION	BD090542.1 GI:22636152	
KEYWORDS	JP 2001342148-A/2.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 714) Serizawa,N., Hanyama,H., Nakahara,K. and Tamaki,I. Drug containing humanized anti-Fas antibody Patent: JP 2001342148-A 2 11-DEC-2001;	
AUTHORS	TAMAKI	
JOURNAL	PC A6IK39./395,A6IK38./00,A6IPJ16,A6IP7./06,A6IP9./00,A6IP9./10, PC A6IP13./12, PC A6IP19./02,A6IP29./00,A6IP37./00,A6IP37./06,A6IP37./08,A6IP43./00// PC C12N15./09, PC A6IK37./02,C12N15./00	
COMMENT	OS Mus musculus (mouse) PN JP 2001342148-A/2 PD 11-DEC-2001 PF 28-MAR-2001 JP 2001093106 PI NOBIFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUO PI TAMAKI	

CC Drug containing humanized anti-Fas antibody  
 FH Key Location/Qualifiers  
 FT CDS (1)..(714)  
 FT mat\_peptide (61)..(714)  
 FT sig\_peptide (1)..(60)  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 BASE COUNT 200 a 184 c 173 g 157 t  
 ORIGIN  
 Query Match 88.8%; Score 293; DB 6; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 1.2e-88;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
 QY 1 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCCACC 60  
 61 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCCACC 120  
 61 ATCTCCTGCAGAGCCCAAGAGTGTGATTTATGATGGTATGTTATG--TGGTAC 117  
 121 ATCTCCTGCAGAGCCCAAGAGTGTGATTTATGATGGTATGTTATGAACTGGTAC 180  
 118 CAACAGAAACGAGAGCCAGCCCAAACTCTCACCCTATGTCATCCATCTAGAAATCT 177  
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 Db 298 ACCTTCGGTGTGGAGCAAGCTGGAGCTGAA 330  
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 BD090651 714 bp DNA linear PAT 27-AUG-2002  
 LOCUS Drug containing humanized anti-Fas antibody.  
 DEFINITION  
 ACCESSION BD090651.1 GI:22636261  
 VERSION BD090651.1  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 714)  
 Takahashi, W., Haruyama, H. and Serizawa, N.  
 Drug containing humanized anti-Fas antibody  
 Patent: JP 2001342149-A 2 11-DEC-2001;  
 SANKYO CO LTD  
 OS Mus musculus (mouse)  
 PN JP 2001342149-A/2  
 PD 11-DEC-2001  
 PI 28-MAR-2001 JP 2001093243  
 REFERENCE WATARU TAKAHASHI, HIDEYUKI HARUYAMA, NOBUFUSA SERIZAWA, PC  
 A61K39/395, A61K39/395, A61P1/16, A61P7/06, A61P9/00, A61P9/10, PC  
 A61P13/12,  
 PC A61P17/00, A61P31/14, A61P31/18, A61P31/20, A61P37/00, A61P37/06,  
 PC A61P37/08,  
 PC A61P43/00//C12N15/02, C12N15/00  
 CC Drug containing humanized anti-Fas antibody  
 FH Key Location/Qualifiers  
 FT CDS (1)..(714)  
 FT mat\_peptide (61)..(714)  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 BASE COUNT 200 a 184 c 173 g 157 t  
 ORIGIN  
 Query Match 88.8%; Score 293; DB 6; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 1.2e-88;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
 QY 1 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCCACC 60  
 61 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCCACC 120  
 61 ATCTCCTGCAGAGCCCAAGAGTGTGATTTATGATGGTATGTTATG--TGGTAC 117  
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 118 CAACAGAAACGAGAGCCAGCCCAAACTCTCACCCTATGTCATCCATCTAGAAATCT 177  
 181 CAACAGAAACGAGAGCCAGCCCAAACTCTCACCCTATGTCATCCATCTAGAAATCT 240  
 178 GGGATCCAGCCAGGTTTATGTTAGTGGAGTGGGCTGGAGACAGACTTCACCCCTCAACATCAT 237  
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 QY 238 CCGTGGAGAGAGATGCTGCACCTATCTACTGTGCACCTTGTATATGAGATCCTCC 297  
 301 CCGTGGAGAGAGATGCTGCACCTATCTACTGTGCACCAAGTAATGAGATCCTCCG 360  
 Db 298 ACCTTCGGTGTGGAGCAAGCTGGAGCTGAA 330  
 361 ACCTTCGGTGTGGAGCAAGCTGGAGAAATCAA 393  
 QY 298 ACCTTCGGTGTGGAGCAAGCTGGAGCTGAA 330  
 361 ACCTTCGGTGTGGAGCAAGCTGGAGAAATCAA 393  
 Db 361 ACCTTCGGTGTGGAGCAAGCTGGAGAAATCAA 393  
 RESULT 5  
 E40005 714 bp DNA linear PAT 31-JAN-2002  
 LOCUS Drug containing anti-Fas antibody.  
 DEFINITION  
 ACCESSION E40005  
 VERSION E40005.1 GI:18627121  
 KEYWORDS JP 2000169393-A/2.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 714)  
 Serizawa, N., Haruyama, H., Takahashi, W., Yoshida, H., Ichikawa, K.,  
 Okuma, T., Otsuki, M., Shiraiishi, A. and Yonehara, S.  
 Drug containing anti-Fas antibody  
 Patent: JP 2000169393-A 2 20-JUN-2000;  
 SANKYO CO LTD  
 OS Mus musculus (mouse)  
 PN JP 2000169393-A/2  
 PD 20-JUN-2000  
 PF 30-SEP-1999 JP 1999278301  
 PR  
 PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI  
 HIROKO YOSHIDA,  
 PI KIMIHISA ICHIKAWA, JUN OKUMA, MASAHIKO OTSUKI, AKIO SHIRAIISHI, PI  
 SHIN YONEHARA  
 PC A61K39/395, A61K39/395, A61K39/00, A61P1/16, A61P7/06, A61P9/00, PC  
 A61P9/10,  
 PC A61P13/12, A61P31/18, A61P37/06, C12N15/10, C12N15/02, C12N15/09, PC  
 C12P21/08//  
 PC C07K16/28, C12N5/00, C12N15/00, C12N15/00  
 CC  
 FH Key Location/Qualifiers  
 FT CDS (1)..(714)  
 FT mat\_peptide (61)..(714)  
 FT sig\_peptide (1)..(60).

FEATURES	source	Location/Qualifiers
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Best Local Similarity	94.6%; Pred. No. 1.2e-88;	
Matches 315; Conservative	0; Mismatches 15; Indels 3; Gaps 1	
OY	1 GACATTGGCTCACCATTTCCTCCACTCTTGTGGCTGTCTCTTAGGCGACGAGGGCCACC 60	
DB		
OY	61 GACATTGGCTGACCCAACTCTCCACTCTTGTGGCTGTCTCTTAGGCGACGAGGGCCACC 120	
DB		
OY	61 ATCTCTTCGAAGGCCAGCCAAAGTGTGATTATGATGGTATGATATG--TGGTAC 117	
DB		
OY	121 ATCTCTTCGAAGGCCAGCCAAAGTGTGATTATGATGGTATGATATGATGACGTGAC 180	
DB		
OY	118 CACGGAAGAACGAGCAGCAGCCAACTCCTCAGCTTATGCTGCATCCAACTAGAACT 177	
DB		
OY	181 CACGGAAGAACGAGCAGCAGCCAACTCCTCAGCTTATGCTGCATCCAACTAGAACT 240	
DB		
OY	178 GGGATCCAGCAGCAGCTTATGTCGAGTGGTGGTGGAGACAGCTTACCTCAACATCCAT 237	
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OY	241 GGGATCCAGCAGCAGCTTATGTCGAGTGGTGGTGGAGACAGCTTACCTCAACATCCAT 300	
DB		
OY	238 CCTGTGAGAGAGAGAGTGTGCAACCTATTACTGTGACGCTTGTATGAGAGATCCTCC 297	
DB		
OY	301 CCTGTGAGAGAGAGAGTGTGCAACCTATTACTGTGACGCAAGTAATGAGAGATCCTCG 360	
DB		
OY	298 ACGTTCCGCTGCTGGACCACTGGAGCTGAAA 330	
DB		
OY	361 ACGTTCCGCTGCTGGACCACTGGAGCTGAAA 393	
DB		
RESULT 6		
E40813		
LOCUS	E40813	714 bp DNA linear PAT 31-JAN-2002
DEFINITION	Humanized anti-Fas antibody.	
ACCESSION	E40813	
VERSION	E40813.1 GI:18627390	
KEYWORDS	JP 200016574-A/2.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 714)	
NOTE	Seizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.	
JOURNAL	Humanized anti-Fas antibody	
COMMENT	Patent: JP 200016574-A 2 20-JUN-2000;	
OS	SANKYO CO LTD	
PN	Mus musculus (mouse)	
PD	JP 200016574-A/2	
PF	20-JUN-2000	
PR	29-SEP-1999 JP 1999275441	
PI	NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUO TAMAKI	
PC	C12N5/09,A61K39/00,A61K39/395,A61P37/02,A61P43/00,	
PC	C07K16/18	
PC	C12N1/21,C12N5/10,C12P21/08/(C12N1/21,C12R1:19),C12N5/00,PC	
CC	C12N5/00	
FH	key	Location/Qualifiers
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FT	mat_peptide	(61)..(714)
FT	sig_peptide	(1)..(60).
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Best Local Similarity	94.6%; Pred.	No. 1.2e-88;
Matches 315; Conservative	0; Mismatches 15; Indels	3; Gaps 1;
OY	1	GACATTGGTCACCACCAATTTCCAGCTTCTTGCGTGTGCTCATAGGGCAGAGGCCACC 60 
Dd	61	GACATTGGTCGACCCAATCTGCACACTCTTTGGCTGTCTCTTAGGGCACAGGGCCCC 120 
OY	61	ATCTCCTCAAAGGCCAACAAAGTGTGATTATGATGGTGAATAGTTATATG---TGGTAC 117 
Dd	121	ATCTCCTCAAAGGCCAACAAAGTGTGATTATGATGGTGAATAGTTATATGTAACGTGTAC 180 
OY	118	CACAGAACAACGAGCAGCAGCCCACCAACTCTCCTCACCTATGCTGCATTCGAATCTAATCT 177 
Dd	181	CACAGAACAACGAGCAGCAGCCCACCAACTCTCCTCATATGCTGCATTCGAATCTAATACT 240 
OY	178	GGGATCCAGCCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237 
Dd	241	GGGATCCAGCCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 300 
OY	238	CCTGGGAGGAGGAGGAGATGCTGCACCAACTATACGTCTGAGCTTGTGAATGAGAGATCTCC 297 
Dd	301	CCTGGGAGGAGGAGGAGATGCTGCACCAACTATACGTCTGAGCAAGTAATGAGATCTCGG 360 
OY	298	ACGTTCCGCTCTGGGACCAACGTGGAGCTGAAA 330 
Dd	361	ACGTTCCGCTCTGGGACCAACGTGGAGCTGAAA 393 
R	E	L
RESULT 7		
E43359		714 bp DNA linear PAT 31-JAN-2002
LOCUS	E43359	Humanized anti-Fas antibody.
DEFINITION	E43359	Humanized anti-Fas antibody.
ACCESSION	E43359.1	GI:18627625
VERSION	JP_2000I166573-A/2.	
KEYWORDS	JP_2000I166573-A/2.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Takahashi,W., Haruyama,H. and Setizawa,N. Humamized anti Fas antibody Patent: JP 20016573-A 2 -JUN-2000;  SANKYO CO LTD OS Mus musculus (mouse) PN JP 2000I166573-A/2 PD 20-JUN-2000 PF 29-SEP-1999 JP 1999275440  PR WAFARU TAKAHASHI, HIDEYUKI HARUYAMA, NOBUKI SERIZAWA PC C12N15/09,A61K38/00,A61K39/00,A61K39/395,A61K39/395,A61P37/00,PC A61P43/00, PC C07H16/28,C12N1/21,C12N5/10,C12N15/02,C12P21/08/(C12P21/08, PC C12R1:91), PC C12N15/00,A61K37/02,C12N5/00,C12N15/00 PC CC Key location/Qualifiers FH CDS (1)..(714) FT mat.peptide (61)..(714) FT sig.peptide (1)..(60). FEATURES Location/Qualifiers source 1..714 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090"	
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Base Count	200 a	184 c    173 g    157 t
Origin		





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QY 238 CCTGTGAGAGAGAGAGAGTCTGCAACCTATTACTGTCAGCTTTGTAATGAGATCCTCC 297  
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DB 307 CCTGTGAGAGAGAGAGAGTCTGCAACCTATTACTGTCAGCAAAAGTAGAGATCCTCCG 366  
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QY 298 ACCTTGGTGTGGAGAGCCAGCTGAGCTGAGAA 330  
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DB 367 ACCTTGGTGTGGAGAGCCAGCTGAGAAATCAAA 399  
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RESULT 10  
E30617 925 bp DNA linear PAT 18-JUN-2001  
LOCUS Antibody and nucleic acid encoding the same.  
DEFINITION  
ACCESSION E30617.1 GI:13017183  
VERSION JP 1999332563-A/4.  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Mitsuhashi, O., Takayuki, K. and Ikuno, M.  
TITLE Antibody and nucleic acid encoding the same  
JOURNAL Patent: JP 1999332563-A 4 07-DEC-1999;  
ASAHII CHEM IND CO LTD  
COMMENT  
OS Mus sp. (mouse)  
PN JP 1999332563-A/4  
PD 07-DEC-1999  
PF 26-MAY-1998 JP 1998163034  
PR  
PI MITSUHASHI ONO, TAKAYUKI KUSAKA, IKUNO MORIMOTO  
PC C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,  
PC C12N15/00,  
PC C12N15/00  
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CC Topology: Linear;  
CC Key  
FH Location/Qualifiers  
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Location/Qualifiers  
1..925  
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Best Local Similarity 94.6%; Pred. No. 1.2e-88;  
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

DB 706 CCTGTGAGAGAGAGAGAGTCTGCAACCTATTACTGTCAGCAAAAGTAGAGATCCTCCG 765  
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QY 298 ACCTTGGTGTGGAGAGCCAGCTGAGCTGAGAA 330  
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DB 766 ACCTTGGTGTGGAGAGCCAGCTGAGAAATCAAA 798  
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RESULT 11  
MUSL71IGKV 354 bp mRNA linear ROD 29-OCT-1994  
LOCUS Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial  
DEFINITION  
ACCESSION M97875.1 GI:198677  
VERSION M97875  
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;  
processed gene.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.  
TITLE Characterization of murine monoclonal anti-CD4: epitope  
recognition, idiotype expression, and variable gene sequence  
JOURNAL Unpublished (1992)  
COMMENT Original source text: Mus musculus (strain BALB/c, sub-species  
domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.  
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Matches 313; Conservative 0; Mismatches 17; Indels 3; Gaps 1;

ACCESSION	region, (Igf) mRNA, partial cds.
VERSION	Af045518
KEYWORDS	Af045518.1 GI:2906119
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 393) O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D. Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies Unpublished
JOURNAL	2 (bases 1 to 393) O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D. Direct Submission Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
AUTHORS	location/Qualifiers
TITLE	1..393
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SOURCE	/strain="C57BL/6"
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	/clone="5G6"
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CDS	/gene="Igf"
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	/gene="Igf"
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	/protein_id="AAC04546.1"
	/db_xref="GI:2906120"
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OY	1 GACATTGGCGTCACCACCAATCTCCAGCTTTGGCTGTCTGAAGGCAGAGGCCACAC 60
Dd	
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Dd	
OY	61 ATCTCTGCAGAAGCGACGCCAAAGTGTGATTATGATGTGATAGTTATATG--TGTAC 117
Dd	
OY	121 ATCTCTGCAGAAGCGACGCCAAAGTGTGATTATGATGTGATAGTTATATGACGTAC 180
Dd	
OY	118 CACAGAAACAGGACAGCACGCCAACAATCTCTACACTATGCTGCATCCAACTAGACATCT 177
Dd	
OY	181 CACAGAAACAGGACAGCACGCCAACAATCTCTATGCTGCATCCAACTAGACATCT 240
Dd	
OY	178 GGATATCCAGCAGAGTTTAGTGGAGAGTGGCTGGGACAGACATTCACCCCAACATCAT 237
Dd	
OY	241 GGGATATCCAGCAGAGTTTAGTGGAGAGTGGCTGGGAGAGACATTCACCCCAACATCAT 300
Dd	
OY	238 CCTGTGAGAGAGAGATGCTCAACCTATTACTGTAGCTTTGATAGAGATCTCC 297
Dd	
OY	301 CCTGTGAGAGAGAGATGCTCAACCTATTACTGTAGCAAAAGTAATGAGATCTCGTG 360
Dd	
OY	298 AC GTTGGTCTGGGAGCCAACTGAGCTGAAA 330
Dd	

Db	361	ACGTTGCGTGGAGGACCAACGCTGGAATCAAA	393
RESULT 14	E07408	333 bp RNA	Linear PAT 29-SEP-1997
LOCUS	E07408		
DEFINITION	cDNA encoding L chain variable region of mouse anti-HIV antibody.		
ACCESSION	E07408		
VERSION	E07408.1	GI:2175547	
KEYWORDS	JP 1994125785-A/4.		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	Eukariota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.		
AUTHORS	1 (bases 1 to 333) Maeda,H., Kurumi,K., Eda,Y., Shiosaki,K., Nagatomi,K. and Tokiyoshi,Y.		
TITLE	RECOMBINANT ANTI-HIV ANTIBODY AND ITS PREPARATION		
JOURNAL	Patent: JP 1994125783-A 4 10-MAY-1994; CHEMO SERO THERAPEUT RES INST		
IENT	OS	Mus sp. (mouse)	
	PN	JP 1994125783-A/4	
	PD	10-MAY-1994	
	PF	28-DEC-1991 JP 1991359808	
	PI	MAEDA HIROAKI, KURUMI KAZUHIKO, EDA YASUYUKI, SHIOSAKI KOICHI, PI	
	NC	NGATOMI KIYOSHI, TOKIYOSHI YUKIO	
	CC	CI2P21/08,A61K39/395,A61K39/395,CI2N15/13,(CI2P21/08, PC	
	CC	CI2R1:91);	
	CC	strandedness: Double;	
	CC	topology: Linear;	
	CC	hypothetical: NO;	
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Best Local Similarity	93.7%;	Pred. No. 5e-87;	
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QY	61	ATCTCCGCAAGGCGACCCAAAGTGTGATTATGATGGTATGTAATG--TGGTAC	117
DB	61	ATCTCCGCAAGGCGACCCAAAGTGTGATTATGATGGTATGTAATGTAATGACTGTAC	120
QY	118	CAACAGAAACCCAGACAGCCCAACCTCCACCTATGCTGCATCCCAATCTAGAACT	177
DB	121	CAACAGAAACCCAGACAGCCCAACCTCCACCTATGCTGCATCCCAATCTAGAACT	180
QY	178	GGGATCCACGACGATTAGTGGCAGTGGGTCTGGCAGACACTTCACCTCACATCAT	237
DB	181	GGGATCCACGACGATTAGTGGCAGTGGGTCTGGCAGACACTTCACCTCACATCAT	240
QY	238	CGTGTGAGGAGGAGATGCTGCAAACTATTACTGTCAGCTTTGTAAAGGATCCGCC	297
DB	241	CGTGTGAGGAGGAGATGCTGCAAACTATTACTGTCAGCAAACTAATGAGATCGCTGG	300

	LOCUS	MAA005355	333 bp	mRNA	linear	ROD 08-FEB-1999
Db	DEFINITION	Mus musculus immunoglobulin variable light chain region.				
	ACCESSION	AJ005355				
	VERSION	AJ005355.1	GI:3046765			
	KEYWORDS	immunoglobulin; light chain; variable region.				
	SOURCE	Mus musculus (house mouse)				
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OY	REFERENCE	Monnet,C., Laune,D., Laroche-Traïneau,J., Biard-Piechaczyk,M., Briant,L., Bes,C., Pugnieri,M., Mani,J.C., Pau,B., Cerutti,M., Devauchelle,G., Devaux,C., Granier,C. and Charles,T. Synthetic peptides derived from the variable regions of an anti-CD4 monoclonal antibody bind to CD4 and inhibit HIV-1 promoter activation in virus-infected cells J. Biol. Chem. 274 (6), 3789-3796 (1999) 99121124 9920932				
JOURNAL TITLE	JOURNAL REFERENCE AUTHORS	Monnet,C., Laune,D., Laroche-Traïneau,J., Piechaczyk,M., Pugnieri,M., Mani,J.C., Pau,B., Cerutti,M., Devauchelle,G., Devaux,C., Granier,C. and Charles,T. Synthetic peptides designed from the variable regions of an anti-CD3 like monoclonal antibody bind to CD4 and inhibit HIV promoter activity Unpublished 3 (bases 1 to 333) Charles,T.				
JOURNAL TITLE	JOURNAL REFERENCE	Direct Submission Submitted (06-APR-1998) Char��es T., Faculte de Pharmacie, CNRS UMR 9921, 15 Avenue Charles Flahault - Montpellier, 34060, FRANCE Location/Qualifiers 1..333				
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Db	121	CACAGAAGCAGAGACGCCAACCTCCTCATCTATGCTGCATCCAATCTAGAATCT	180			
OY	178	GGGATCCCAGCAGGTTTAAATGGCGAGTGGTCTGGGACAGACTTCACCTCAACATCAT	237			
Db	181	GGGATCCCAGCAGGTTTAAATGGCGAGTGGTCTGGGACAGACTTCACCTCAACATCAT	240			

Qy 238 CCTGTGAGAGAGAGATGCTGCAACCTATTAAGTCAAGCTTTGTAATGAGGATCCTCCC 297  
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Qy 298 ACCTTCGGTGTGCTGGACCAAGCTGGAGCTGAAA 330  
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Db 301 ACCTTCGGTGTGAGGACCAAGCTGGAAATCAAA 333  
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## OM protein - protein search, using sw model

Run on: September 10, 2003, 17:39:02; Search time 13.05 Seconds  
(without alignments)  
29.180 Million cell updates/sec

Title: US-09-759-112a-36

Perfect score: 54

Sequence: 1 OLCNEDPPT 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:\*

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- 4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	38	70.4	111	2	US-08-483-632-73
5	38	70.4	111	2	US-08-483-632-73
6	38	70.4	131	1	US-08-137-117D-33
7	38	70.4	131	2	US-08-436-717-33
8	38	70.4	131	2	US-08-621-751A-10
9	38	70.4	131	2	US-08-621-751A-14
10	38	70.4	131	2	US-08-483-636-58
11	38	70.4	131	2	US-08-483-632-58
12	38	70.4	132	2	US-08-483-632-2
13	38	70.4	132	2	US-08-483-632-2
14	36	66.7	77	2	US-08-465-380-4
15	36	66.7	77	2	US-08-465-380-4
16	36	66.7	77	2	US-08-480-478-33
17	36	66.7	77	2	US-08-486-397-4
18	36	66.7	77	2	US-08-486-397-4
19	36	66.7	77	2	US-08-486-399-4
20	36	66.7	77	2	US-08-486-399-4
21	36	66.7	77	2	US-08-461-965-4
22	36	66.7	77	2	US-08-461-965-4
23	36	66.7	77	2	US-08-326-110A-33
24	36	66.7	77	2	US-08-634-641-4
25	36	66.7	77	2	US-08-634-641-4
26	36	66.7	77	3	US-09-249-471-4
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31	36	66.7	77	3	US-09-249-451-40	Sequence 40, Appli
32	36	66.7	77	3	US-08-809-455-4	Sequence 4, Appli
33	36	66.7	77	3	US-08-809-455-40	Sequence 40, Appli
34	36	66.7	77	3	US-09-249-461-4	Sequence 4, Appli
35	36	66.7	77	3	US-09-249-461-40	Sequence 40, Appli
36	36	66.7	77	3	US-09-249-448-4	Sequence 4, Appli
37	36	66.7	77	3	US-09-249-448-40	Sequence 40, Appli
38	36	66.7	77	4	US-09-249-473-4	Sequence 4, Appli
39	36	66.7	77	4	US-09-249-473-40	Sequence 40, Appli
40	36	66.7	81	2	US-08-465-380-7	Sequence 7, Appli
41	36	66.7	81	2	US-08-480-478-36	Sequence 36, Appli
42	36	66.7	81	2	US-08-486-397-7	Sequence 7, Appli
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44	36	66.7	81	2	US-08-461-965-7	Sequence 7, Appli
45	36	66.7	81	2	US-08-326-110A-36	Sequence 36, Appli

## ALIGNMENTS

RESULT 1  
US-08-984-277-7  
Sequence 7, Application US/08984277  
Patent No. 6057421  
GENERAL INFORMATION:  
APPLICANT: Kohler, Sybille  
TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE MONOCLONAL ANTIBODY 1F7  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDermott, Will & Emery  
STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,277  
FILING DATE: 3-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bucca, Daniel  
REGISTRATION NUMBER: 42,368  
REFERENCE/DOCKET NUMBER: 50200-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-756-8600  
TELEFAX: 202-756-8699  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-984-277-7  
Query Match 100.0%; Score 54; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 OLCNEDPT 18

## RESULT 2

US-08-483-636-20

Sequence 20, Application US/08483636

Patent No. 5914110

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P.O. Box 1539 / UM2220

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,636

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-636-20

Query Match 70.4%; Score 38; DB 2; Length 9;

Best Local Similarity 77.8%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OLCNEDPT 9

Db 1 QOSNEDPT 9

## RESULT 3

US-08-483-632-20

Sequence 20, Application US/08483632

Patent No. 5928904

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P.O. Box 1539 / UM2220

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,632

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-632-20

Query Match 70.4%; Score 38; DB 2; Length 9;

Best Local Similarity 77.8%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OLCNEDPT 9

Db 1 QOSNEDPT 9

## RESULT 4

US-08-483-636-73

Sequence 73, Application US/08483636

Patent No. 5914110

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P.O. Box 1539 / UM2220

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:



MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-483-636-73

Query Match 70.4%; Score 38; DB 2; Length 111;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QUCNEDPPT 9  
DB 93 QOSNEDPPT 101

RESULT 5  
US-08-483-632-73  
Sequence 73, Application US/08483632  
Patent No. 5928904  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSER: Intellectual Property  
STREET: P.O. Box 1539 / UM2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-483-632-73

Query Match 70.4%; Score 38; DB 2; Length 111;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QUCNEDPPT 9  
DB 93 QOSNEDPPT 101

RESULT 6  
US-08-137-117D-33  
Sequence 33, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-33

Query Match 70.4%; Score 38; DB 1; Length 131;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9  
DB 113 QOSNEDPPT 121

US-08-436-717-33  
Sequence 33, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Maayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436, 717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137, 117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-33

Query Match 70.4%; Score 38; DB 2; Length 131;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9  
DB 113 QOSNEDPPT 121

RESULT 8  
US-08-621-751A-10  
Sequence 10, Application US/08621751A  
Patent No. 5882644  
GENERAL INFORMATION:  
APPLICANT: Chang, Chung N.  
APPLICANT: Landolfi, Nicholas F.  
APPLICANT: Martin, Ulrich  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER LLP  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621, 751A  
FILING DATE: 22-MAR-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 321152000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141 MRSN FOERS SFO  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-621-751A-10

Query Match 70.4%; Score 38; DB 2; Length 131;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9  
DB 113 QOSNEDPPT 121

RESULT 9  
US-08-621-751A-14  
Sequence 14, Application US/08621751A  
Patent No. 5882644  
GENERAL INFORMATION:  
APPLICANT: Chang, Chung N.  
APPLICANT: Landolfi, Nicholas F.

APPLICANT: Martin, Ulrich  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND  
METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS: 17  
ADDRESS: MORRISON & FOERSTER LLP  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,751A  
FILING DATE: 22-MAR-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 321152000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141 MRSN FOERS SFO  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-621-751A-14

Query Match 70.4%; Score 38; DB 2; Length 131;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLCNEDPPT 9  
Db 113 QOSNEDPPT 121

RESULT 10  
US-08-636-58  
Sequence 58, Application US/08483636  
Patent No. 5914110  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESS: Intellectual Property  
STREET: P.O. Box 1539 / UM2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-636-58

Query Match 70.4%; Score 38; DB 2; Length 131;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLCNEDPPT 9  
Db 112 QOSNEDPPT 120

RESULT 11  
US-08-483-632-58  
Sequence 58, Application US/08483632  
Patent No. 5928904  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESS: Intellectual Property  
STREET: P.O. Box 1539 / UM2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-632-58

Query Match 70.4%; Score 38; DB 2; Length 131;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9  
Db 112 QOSNEDDPT 120

RESULT 12  
US-08-483-636-2  
Sequence 2, Application US/08483636  
Patent No. 5914110  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Groves, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
OPERATING SYSTEM: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
STREET: P.O. Box 1539 / UM2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-636-2

Query Match 70.4%; Score 38; DB 2; Length 132;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9  
Db 113 QOSNEDDPT 121

RESULT 13  
US-08-483-632-2  
Sequence 2, Application US/08483632  
Patent No. 5928904  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Groves, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
OPERATING SYSTEM: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
STREET: P.O. Box 1539 / UM2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-632-2

Query Match 70.4%; Score 38; DB 2; Length 132;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9  
Db 113 QOSNEDDPT 121

RESULT 14  
US-08-465-380-4

Sequence 4, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssemaus, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 213/268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 955-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
8-465-380-4

Query Match 66.7%; Score 36; DB 2; Length 77;  
Best Local Similarity 83.3%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEBPP 8  
DB 25 CNEBPP 30

RESULT 15  
US-08-465-380-40  
Sequence 40, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssemaus, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 213/268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 955-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-08-465-380-40

Query Match 66.7%; Score 36; DB 2; Length 77;  
Best Local Similarity 83.3%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEBPP 8  
DB 25 CNEBPP 30

Search completed: September 10, 2003, 17:43:23  
Job time : 14.05 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2003, 17:42:07 ; Search time 18 Seconds  
(without alignments)  
72.956 Million cell updates/sec

Title: US-09-759-112a-36

Perfect score: 54

Sequence: 1 OLCNDDPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	9	11	US-09-759-112a-36
2	54	100.0	110	11	US-09-759-112a-24
3	41	75.9	407	14	US-10-085-108-26
4	39	72.2	399	9	US-09-729-674-94
5	38	70.4	9	10	US-09-879-461-20
6	38	70.4	112	10	US-09-144-886-80
7	38	70.4	131	10	US-09-879-461-58
8	38	70.4	132	10	US-09-879-461-2
9	38	70.4	272	15	US-10-207-655-112
10	36	66.7	77	11	US-09-498-272-4
11	36	66.7	77	11	US-09-498-272-40
12	36	66.7	81	11	US-09-498-272-7
13	36	66.7	100	11	US-09-498-272-20
14	36	66.7	141	11	US-09-764-891-3695
15	36	66.7	181	15	US-10-156-761-7554

16	35	64.8	356	12	US-10-017-161-1738	Sequence 1738, Ap
17	35	64.8	402	10	US-09-738-626-5344	Sequence 5344, Ap
18	35	64.8	491	11	US-09-999-2208-4	Sequence 4, Appl
19	35	64.8	731	10	US-09-981-423-2	Sequence 2, Appl
20	35	64.8	1420	10	US-09-801-368-356	Sequence 356, App
21	34	63.0	377	9	US-09-849-031A-3	Sequence 3, Appl
22	34	63.0	377	9	US-09-849-562A-3	Sequence 3, Appl
23	34	63.0	377	12	US-10-329-068-3	Sequence 3, Appl
24	34	63.0	543	10	US-09-925-300-1700	Sequence 1700, Ap
25	33	61.1	9	10	US-09-879-461-28	Sequence 28, Ap
26	33	61.1	10	11	US-09-563-222-34	Sequence 34, Appl
27	33	61.1	70	14	US-10-068-347-12	Sequence 12, Appl
28	33	61.1	80	11	US-09-764-891-3444	Sequence 3444, Ap
29	33	61.1	91	9	US-09-864-761-48847	Sequence 48847, A
30	33	61.1	112	12	US-10-160-506-81	Sequence 81, Appl
31	33	61.1	116	9	US-09-764-869-689	Sequence 689, App
32	33	61.1	116	15	US-10-091-504-689	Sequence 689, App
33	33	61.1	131	10	US-09-879-461-14	Sequence 14, Appl
34	33	61.1	144	9	US-09-784-810A-8	Sequence 8, Appl
35	33	61.1	148	9	US-09-867-550-544	Sequence 544, App
36	33	61.1	176	12	US-10-259-165-86	Sequence 86, Appl
37	33	61.1	176	12	US-10-259-165-346	Sequence 346, App
38	33	61.1	176	14	US-10-078-929-86	Sequence 86, Appl
39	33	61.1	196	15	US-10-189-346-4	Sequence 4, Appl
40	33	61.1	200	11	US-09-227-488-1	Sequence 1, Appl
41	33	61.1	200	15	US-10-189-346-31	Sequence 31, Appl
42	33	61.1	200	15	US-10-189-346-32	Sequence 32, Appl
43	33	61.1	201	15	US-10-189-346-29	Sequence 29, Appl
44	33	61.1	201	15	US-10-189-346-30	Sequence 30, Appl
45	33	61.1	280	12	US-10-259-165-174	Sequence 174, App

## ALIGNMENTS

RESULT 1  
US-09-759-112a-36  
; Sequence 36, Application US/09759112A  
; Publication No. US20030100741A1  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT  
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1E7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE  
; FILE REFERENCE: 200-013  
; CURRENT APPLICATION NUMBER: US/09/759,112A  
; CURRENT FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-759-112a-36

Query Match 100.0%; Score 54; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.8e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OLCNDDPT 9  
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Db 1 OLCNDDPT 9

RESULT 2  
US-09-759-112a-24  
; Sequence 24, Application US/09759112A  
; Publication No. US20030100741A1  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT

TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE  
TITLE OF INVENTION: ANTIBODIES  
FILE REFERENCE: 200-013  
CURRENT APPLICATION NUMBER: US/09/759,112A  
CURRENT FILING DATE: 2001-01-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 24  
LENGTH: 110  
TYPE: PRT  
ORGANISM: mouse  
US-09-759-112a-24

Query Match 100.0%; Score 54; DB 11; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNDDPPT 9  
:|||||  
92 QLCNDDPPT 100

RESULT 3  
US-10-085-108-26  
Sequence 26, Application US/10085108  
Publication No. US2002017685A1  
GENERAL INFORMATION:  
APPLICANT: LUCAS, Sophie; BOON-PALIEUR, Thierry  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING  
FOR  
TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C  
MAGE-B FAMILIES AND USES THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Publight & Jaworski L.L.P.  
STREET: 666 Fifth Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/085,108  
FILING DATE: 01-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/501,104  
FILING DATE: 09-Feb-2000  
APPLICATION NUMBER: 09/468,433  
FILING DATE: December 17, 1999  
APPLICATION NUMBER: 09/066,281  
FILING DATE: April 24, 1998  
APPLICATION NUMBER: 08/845,528  
FILING DATE: April 25, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 318-3100  
TELEFAX: (212) 318-3400  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 407  
TYPE: amino acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-085-108-26

Query Match 75.9%; Score 41; DB 14; Length 407;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCNDDPPT 8  
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Db 346 QVCNSDDPPT 353

RESULT 4  
US-09-729-674-94  
Sequence 94, Application US/09729674  
Patent No. US2001003935A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavallie, Edward R.  
APPLICANT: Collins-Racie, Lisa A.  
APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Agostino, Michael J.  
APPLICANT: Steininger II, Robert J.  
APPLICANT: Spaulding, Vikki  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fechtel, Kim  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
FILE REFERENCE: 6055-64X  
CURRENT APPLICATION NUMBER: US/09/729,674  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: 09/539,330  
PRIOR FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 283  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 94  
LENGTH: 399  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-729-674-94

Query Match 72.2%; Score 39; DB 9; Length 399;  
Best Local Similarity 62.5%; Pred. No. 68;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNDDPPT 9  
:|||||  
Db 279 MCDPDDPPT 286

RESULT 5  
US-09-879-461-20  
Sequence 20, Application US/09879461  
Publication No. US20020193575A1  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: Corporate Intellectual Property, UW2220 - 709  
Swedeland Rd.  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,461  
FILING DATE: 12-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,929  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/136,783  
FILING DATE: 14-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-879-461-20

Query Match 70.4%; Score 38; DB 10; Length 9;  
Best Local Similarity 77.8%; Pred. No. 4.8e+05;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9  
| |||||  
Db 1 QOSNEDPPT 9

RESULT 6  
US-09-144-886-80  
Sequence 80, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amerisderfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
TITLE OF INVENTION: Botulinum Neurotoxins  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 80  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
OTHER INFORMATION: 1B6 region VL epitope 1  
US-09-144-886-80

Query Match 70.4%; Score 38; DB 10; Length 112;  
Best Local Similarity 77.8%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9  
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Db 93 QOSNEDPPT 101

RESULT 7  
US-09-879-461-58  
Sequence 58, Application US/09879461  
Publication No. US20020193575A1

GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
Gross, Mitchell S.  
Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: Corporate Intellectual Property, UM2220 - 709  
Swedeland Rd.  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,461  
FILING DATE: 12-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,929  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/136,783  
FILING DATE: 14-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-09-879-461-58

Query Match 70.4%; Score 38; DB 10; Length 131;  
Best Local Similarity 77.8%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9  
| |||||  
Db 112 QOSNEDPPT 120

RESULT 8  
US-09-879-461-2  
Sequence 2, Application US/09879461  
Publication No. US20020193575A1  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
Gross, Mitchell S.  
Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: Corporate Intellectual Property, UM2220 - 709  
Swedeland Rd.  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/879,461
  FILING DATE: 12-Jun-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/612,929
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 08/136,783
  FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Sutton, Jeffrey A.
  REGISTRATION NUMBER: 34,028
  REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (215) 270-5024
  TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  LENGTH: 132 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2

Query Match          70.4%; Score 38; DB 10; Length 132;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPP 9
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Db 113 QCSNEDPP 121

RESULT 9
US-10-207-655-172
Sequence 172, Application US/10207655
GENERAL INFORMATION:
  APPLICANT: Ledbetter, Jeffrey A.
  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
  FILE REFERENCE: 390069,401C1
  CURRENT APPLICATION NUMBER: US/10/207,655
  CURRENT FILING DATE: 2002-07-25
  NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
  SEQ ID NO 172
  LENGTH: 272
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-207-655-172

Query Match          70.4%; Score 38; DB 15; Length 272;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDPP 8
   |||||
Db 22 ELCDDDPP 29

RESULT 10
US-09-498-272-4
Sequence 4, Application US/09498272
GENERAL INFORMATION:
  APPLICANT: Vlaauk, George Phillip
```

```

Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Ganssemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Lyon & Lyon
  STREET: 633 West Fifth Street
  CITY: Suite 4700
  STATE: Los Angeles
  COUNTRY: U.S.A.
  ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/498,272
  FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US95/13231
  FILING DATE: October 17, 1995
  APPLICATION NUMBER: 08/466,399
  FILING DATE: June 5, 1995
  APPLICATION NUMBER: 08/466,397
  FILING DATE: June 5, 1995
  APPLICATION NUMBER: 08/465,380
  FILING DATE: June 5, 1995
  APPLICATION NUMBER: 08/461,965
  FILING DATE: June 5, 1995
  APPLICATION NUMBER: 08/326,110
  FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
  NAME: BIGGS, SUZANNE L.
  REGISTRATION NUMBER: 30,158
  REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 489-1600
  TELEFAX: (213) 955-0440
  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
  LENGTH: 77 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
  ORGANISM: Ancylostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-498-272-4

Query Match          66.7%; Score 36; DB 11; Length 77;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPP 8
   |||||
Db 25 CNEDEPP 30

RESULT 11
US-09-498-272-40
Sequence 40, Application US/09498272
```

Publication No. US20030113890A1  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
Stanssens, Patrick Eric Hugo  
Messens, Joris Hilda Lieven  
Lauwereys, Marc Josef  
Laroche, Yves Rene  
Jespers, Laurent Stephane  
Ganssemans, Yannick Georges Jozef  
Moyle, Matthew  
Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
INHIBITORS AND ANTICOAGULANT  
PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-498-272-40  
Query Match 66.7%; Score 36; DB 11; Length 77;  
Best Local Similarity 83.3%; Pred. No. 44;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 CNEPPP 8  
|||:|  
DB 25 CNEPPP 30

RESULT 12  
US-09-498-272-7  
Sequence 7, Application US/09498272  
Publication No. US20030113890A1  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
Stanssens, Patrick Eric Hugo  
Messens, Joris Hilda Lieven  
Lauwereys, Marc Josef  
Laroche, Yves Rene  
Jespers, Laurent Stephane  
Ganssemans, Yannick Georges Jozef  
Moyle, Matthew  
Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
INHIBITORS AND ANTICOAGULANT  
PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-498-272-7  
Query Match 66.7%; Score 36; DB 11; Length 81;  
Best Local Similarity 83.3%; Pred. No. 46;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 CNEPPP 8  
|||:|

Db 29 CNEEP 34

RESULT 13  
US-09-498-272-20; Sequence 20, Application US/09498272  
; Publication No. US20030113890A1

; GENERAL INFORMATION:

APPLICANT: Vlaauk, George Phillip

Stanssens, Patrick Eric Hugo

Messens, Joris Hilda Lieven

Lauwereys, Marc Josef

Laroche, Yves Rene

Jespers, Laurent Stephane

Ganssens, Yannick Georges Jozef

Moyle, Matthew

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

INHIBITORS AND ANTICOAGULANT

PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Filth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498.272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 100 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-498-272-20

Query Match 66.7%; Score 36; DB 11; Length 100;  
Best Local Similarity 83.3%; Pred. No. 57;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;Oy 3 CNEDEPT 8  
Db 48 CNEEP 53RESULT 14  
US-09-764-891-3695

; Sequence 3695, Application US/09764891

; Publication No. US20030077808A1

; GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3695

LENGTH: 141

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (78)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (90)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (102)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-891-3695

Query Match 66.7%; Score 36; DB 11; Length 141;  
Best Local Similarity 66.7%; Pred. No. 79;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;Oy 1 QLCNEDEPT 9  
Db 26 QWCCEPPT 34RESULT 15  
US-10-156-761-7554

; Sequence 7554, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 7554

LENGTH: 181

TYPE: PRT

ORGANISM: Streptomyces avermitilis

US-10-156-761-7554

Query Match 66.7%; Score 36; DB 15; Length 181;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches	6;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2	LCNDDPPT	9						
Db	67	LCQBGPPPT	74						

Search completed: September 10, 2003, 17:50:28  
 Job time : 19 secs

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PT region of an anti-idiotypic antibody that binds to human or primate  
 PT anti- human immunodeficiency virus (HIV) antibodies, for use in  
 PT vaccines against HIV -

XX Claim 4; Page 27; 27pp; English.

XX The present invention relates to coding sequences of the murine 1F7  
 CC anti-idiotypic antibody complementarity-determining region (CDR) or  
 CC framework-determining region (FR). The antibody binds to human or primate  
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
 CC treatment of HIV infection. The present sequence is a region of the 1F7  
 CC light chain.

XX Sequence 9 AA;

Query Match 100.0%; Score 54; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 OLCNEDPPT 9  
 |||||  
 1 OLCNEDPPT 9

RESULT 2  
 AA91016  
 ID AAY91016 standard; protein; 28 AA.

XX AAY91016;

XX 05-SEP-2000 (first entry)

XX 1F7 antibody variable light chain L3 amino acid sequence SEQ ID NO:7.

KM 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;  
 KM AIDS; anti-HIV; human immunodeficiency virus; detection;  
 KM acquired immunodeficiency syndrome.

OS Mus sp.

XX US6057421-A.

XX 02-MAY-2000.

XX 03-DEC-1997; 97US-0984277.

XX 30-NOV-1994; 94US-0351193.

XX (IMMP-) IMPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2000-338622/29.

PT Variable heavy and light chain regions of murine monoclonal antibody  
 PT 1F7, useful for treating HIV infection and AIDS -

XX Claim 1; Fig 8; 45pp; English.

XX The present invention describes the variable heavy and light chain  
 CC regions (1) of murine monoclonal antibody (mAb) 1F7. AAY91014 to  
 CC AAY91016 represent specifically claimed amino acid sequences of the  
 CC variable light chain, and AAY91017 to AAY91019 represent specifically  
 CC claimed amino acid sequence of the variable heavy chain. The antibodies  
 CC are used for treatment of HIV (human immunodeficiency virus) infection  
 CC and AIDS (acquired immunodeficiency syndrome). They are also used for  
 CC detecting HIV in serum and for stimulating HIV antigen related and  
 CC committed B cells to produce broadly reactive and neutralising antibodies  
 CC by clonotypic stimulation.

XX Sequence 28 AA;

Query Match 100.0%; Score 54; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OLCNEDPPT 9  
 |||||  
 Db 10 OLCNEDPPT 18

RESULT 3  
 AA018536  
 ID AA018536 standard; Protein; 110 AA.

XX AA018536;

XX 11-OCT-2002 (first entry)

XX Murine Mab 1F7 light chain.

XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
 KM complementarity determining region; framework-determining region;  
 KM FR; heavy chain; light chain; HIV infection.

OS Mus sp.

XX WO200255668-A2.

XX 18-JUL-2002.

XX 11-JUN-2002; 2002MO-US00927.

XX 11-JAN-2001; 2001US-0759112.

XX (IMMP-) IMPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2002-590668/63.

XX N-PSDB; AAL48661.

PT New polynucleotide encoding a complementarity- or framework-determining  
 PT region of an anti-idiotypic antibody that binds to human or primate  
 PT anti- human immunodeficiency virus (HIV) antibodies, for use in  
 PT vaccines against HIV -

XX Claim 9; Page 23-24; 27pp; English.

XX The present invention relates to coding sequences of the murine 1F7  
 CC anti-idiotypic antibody complementarity-determining region (CDR) or  
 CC framework-determining region (FR). The antibody binds to human or primate  
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
 CC treatment of HIV infection. The present sequence is the 1F7 light chain.

XX Sequence 110 AA;

Query Match 100.0%; Score 54; DB 23; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 0.067;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OLCNEDPPT 9  
 |||||  
 Db 92 OLCNEDPPT 100

RESULT 4  
 AB008934  
 ID AB008934 standard; Protein; 407 AA.

XX AB008934;

XX 05-JUN-2003 (first entry)

XX Human tumour rejection antigen precursor, MAGE-B6.



TRAP; tumour rejection antigen precursor; cytolytic T-cell; CTL; tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor; head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma; cutaneous melanoma; nonsmall cell lung cancer; MAGS-B6; human.

OS Homo sapiens.

XX US2002176865-A1.

XX PD 28-NOV-2002.

XX 01-MAR-2002; 2002US-0085108.

XX 09-FEB-2000; 2000US-0501104.

XX 25-APR-1997; 97US-0845528.

XX 24-APR-1998; 98US-0066281.

XX 17-DEC-1999; 99US-0468433.

XX (LUCAS/) LUCAS S.

XX (BOON/) BOON-FALLEUR T.

XX Lucas S, Boon-Falleur T;

XX WPI; 2003-328468/31.

XX N-PSDB; ABX95008.

XX Novel isolated nucleic acid encoding tumor rejection antigen precursor

XX MAGS-C3, MAGS-B5, or MAGS-B6, useful as diagnostic probes to determine

XX presence of abnormal e.g., tumor cells expressing MAGS-C1, MAGS-B5 or

XX MAGS-B6

XX Example 13; Fig 10; 59pp; English.

XX The invention relates to an isolated nucleic acid molecule which encodes

XX a tumour rejection antigen precursor (TRAP) having an amino acid sequence

XX of a TRAP encoded by a fully defined MAGS-C3, MAGS-B5, or MAGS-B6

XX polynucleotide sequence. Also disclosed is a method which is useful for

XX determining presence of cytolytic T-cells specific for complexes of human

XX leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a

XX cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is

XX useful as a diagnostic probe to determine the presence of abnormal

XX (tumour) cells such as seminoma, bladder transitional-cell carcinoma,

XX head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,

XX cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express

XX MAGS-C1, MAGS-B5 or MAGS-B6. The nucleic acid is useful for diagnosing a

XX disorder characterised by expression of MAGS-C1, MAGS-B5 or MAGS-B6 TRAPs

XX or tumour rejection antigens (TRAs). The present sequence represents the

XX amino acid sequence of the human tumour rejection antigen precursor,

XX MAGS-B6.

XX SQ Sequence 407 AA;

XX Query Match 75.9%; Score 41; DB 24; Length 407;

XX Best Local Similarity 75.0%; Pred. No. 43;

XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 QLCNEDPP 8

XX Db 346 QVCNSDDP 353

XX RESULT 5

XX ABG23972

XX ID ABG23972 standard; Protein; 54 AA.

XX AC ABG23972;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #23963.

XX XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS88159.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity

XX Claim 20; SEQ ID NO 54331; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX and gene mapping, and in recombinant production of (II). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (I) is useful in gene therapy techniques

XX to restore normal activity of (II) or to treat disease states involving

XX (II). (II) is useful for generating antibodies against it, detecting or

XX quantitating a polypeptide in tissue, as molecular weight markers and as

XX a food supplement. (II) and its binding partners are useful in medical

XX imaging of sites expressing (II). (I) and (II) are useful for treating

XX disorders involving aberrant protein expression or biological activity.

XX The polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. ABG00010-ABG30377 represent novel human

XX CC diagnostic amino acid sequences of the invention.

XX Note: The sequence data for this patent did not appear in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 54 AA;

XX Query Match 72.2%; Score 39; DB 22; Length 54;

XX Best Local Similarity 75.0%; Pred. No. 14;

XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX QY 2 LCNEDPPT 9

XX Db 7 LCEKDPPT 14

XX RESULT 6

XX ABP09856

XX ID ABP09856 standard; Protein; 54 AA.

XX AC ABP09856;

XX DT 24-JUN-2002 (first entry)

XX DE Human ORFX protein sequence SEQ ID NO:19694.

XX XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

XX KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

XX KW degenerative disorder; osteoarthritis; neurodegenerative disorder;

XX KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.  
 OS Homo sapiens.  
 PN WO200192523-A2.  
 PD 06-DEC-2001.  
 XX  
 PF 29-MAY-2001; 2001WO-US10836.  
 XX  
 PR 30-MAY-2000; 2000US-206132P.  
 PR 29-AUG-2000; 2000US-228716P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PI Shimkete RA, Leach MD;  
 PI N-PSDB; ABN25608.  
 PS WPI: 2002-106308/14.  
 PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders -  
 PS Disclosure; SEQ ID 19694; 1037pp; English.  
 CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-1191 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 54 AA;  
 QY Query Match 72.2%; Score 39; DB 23; Length 54;  
 DB Best Local Similarity 66.7%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QLCNEDPPT 9  
 |||: |||  
 DB 39 QLCQDSPPT 47  
 RESULT 7  
 ABG20915  
 ID ABG20915 standard; Protein; 70 AA.  
 XX  
 AC ABG20915;  
 DT 13-FEB-2002 (first entry)

XX  
 DE Novel human diagnostic protein #20906.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 OS Homo sapiens.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Drmanac RT, Liu C, Tang YT;  
 PI WPI: 2001-639362/73.  
 DR N-PSDB; AAS65102.  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 PS Claim 20; SEQ ID No 51274; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantifying a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostic, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG3037 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 70 AA;  
 QY Query Match 72.2%; Score 39; DB 22; Length 70;  
 DB Best Local Similarity 75.0%; Pred. No. 18;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LCNEDPPT 9  
 |||: |||  
 DB 19 LCEKDPPT 26  
 RESULT 8  
 ABG15042  
 ID ABG15042 standard; Protein; 73 AA.  
 XX  
 AC ABG15042;  
 XX  
 DT 18-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #15033.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 OS WO200175067-A2.  
 PN 11-OCT-2001.  
 PD 30-MAR-2001; 2001WO-US08631.  
 PF 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Drmanac RT, Liu C, Tang YT;  
 PI WPI; 2001-639362/73.  
 PS N-PSDB; AAS79229.

PT -New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

PS Claim 20; SEQ ID No 45401; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 73 AA;  
 SQ

Query Match 72.2%; Score 39; DB 22; Length 73;  
 Best Local Similarity 75.0%; Pred. No. 19;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEBDPT 9  
 ||:|||||  
 Db 19 LCEKDPPT 26

RESULT 9  
 ABG18578  
 ID ABG18578 standard; Protein; 73 AA.  
 XX  
 AC ABG18578;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #18569.  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX

KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 OS WO200175067-A2.  
 PN 11-OCT-2001.  
 PD 30-MAR-2001; 2001WO-US08631.  
 PF 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Drmanac RT, Liu C, Tang YT;  
 PI WPI; 2001-639362/73.  
 PS N-PSDB; AAS82765.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

PS Claim 20; SEQ ID No 48937; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 73 AA;  
 SQ

Query Match 72.2%; Score 39; DB 22; Length 73;  
 Best Local Similarity 75.0%; Pred. No. 19;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEBDPT 9  
 ||:|||||  
 Db 19 LCEKDPPT 26

RESULT 10  
 ABG19791  
 ID ABG19791 standard; Protein; 74 AA.  
 XX  
 AC ABG19791;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #19782.  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX

OS Homo sapiens.  
XX WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
PF 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
PR  
XX (HYSE-) HYSEQ INC.  
PA  
PI Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS68297.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
diagnostics, forensics, gene mapping, identification of mutations  
responsible for genetic disorders or other traits and to assess  
biodiversity -

XX Claim 20; SEQ ID No 50150; 103bp; English.

PS The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 74 AA;

XX Query Match 72.2%; Score 39; DB 22; Length 74;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9  
Db 19 LCEKDPPT 26

RESULT 11  
ABG04110  
ID ABG04110 standard; Protein; 77 AA.  
XX  
AC ABG04110;  
XX  
DT 13-FEB-2002 (first entry)  
XX

XX Novel human diagnostic protein #4101.  
DE  
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX

PN WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
PF 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
PR  
XX (HYSE-) HYSEQ INC.  
PA  
PI Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS68297.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
diagnostics, forensics, gene mapping, identification of mutations  
responsible for genetic disorders or other traits and to assess  
biodiversity -

XX Claim 20; SEQ ID No 34469; 103bp; English.

PS The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 77 AA;

XX Query Match 72.2%; Score 39; DB 22; Length 77;  
Best Local Similarity 75.0%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9  
Db 24 LCEKDPPT 31

RESULT 12  
ABG23982  
ID ABG23982 standard; Protein; 78 AA.  
XX  
AC ABG23982;  
XX  
DT 18-FEB-2002 (first entry)  
XX

XX Novel human diagnostic protein #23973.  
DE  
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX

XX WO200175067-A2.  
XX



PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HYSEQ INC.
PA	
P1	Drmamac RT, Liu C, Tang YT;
DR	WPI; 2001-639362/73.
DR	N-PsDB; AAS82811.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PS	Claim 20; SEQ ID No 48983; 103bp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (II) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or as
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. ABG00010-ABG30377 represent novel human
CC	diagnostic amino acid sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences..
XX	
SQ	Sequence 118 AA:
Query Match	72.2%; Score 39; DB 22; Length 118;
Best Local Similarity	75.0%; Pred No. 30;
Matches 6; Conservativity 1; Mismatches 1; Indels 0; Gaps 0.	
OY	2 LCNEDDPT 9     
DB	65 LCEKDPT 72
BLAST 15	
AAV74157	AAV74157 standard; Protein; 284 AA.
XX	
AC	AAV74157;
DT	14-MAR-2000 (first entry)
XX	
DE	Human prostate tumor EST fragment derived protein #344.
XX	
KW	Pancreas; tumor; EST; expressed sequence tag: human; cytostatic; treatment.
OS	Homo sapiens.
PN	DE19820190-A1.
PD	04-NOV-1999.
PF	28-APR-1998; 98DE-1020190.
BR	28-APR-1998; 98DE-1020190.
XX	

```

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI; 1999-621386/54.
DR N-PSDB; AAZ52971.
XX
PT New human nucleic acid sequences from pancreatic tumors, and related
PT proteins
XX
PS Claim 23; Page 452; 502pp; German.
XX
CC This invention describes novel polypeptides and their encoding nucleic
CC acids derived from human pancreatic tumor tissue which have cytostatic
CC activity. The sequences are also useful in producing pharmaceutical
CC compositions for treatment of pancreatic tumors. AAY73814-Y74252
CC represent protein fragments encoded by the human pancreatic tumor CDNA
CC library derived expressed sequence tag (EST) sequences represented in
CC AAY52858-253014.
XX
SQ Sequence 284 AA;

Query Match 72.2%; Score 39; DB 20; Length 284;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 2 LCNEDPPT 9
   ::::||||
Db 164 MCDDDPPT 171

```

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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:37:57 ; Search time 25.2 seconds  
(without alignments)  
92.162 Million cell updates/sec

Title: US-09-759-112a-36

Perfect score: 54

Sequence: 1 QLCNEDEPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_23.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	81.5	227	5 Q9N8Y0	Q9N8Y0 trypanosoma
2	42	77.8	1009	3 Q74378	Q74378 schizosacch
3	41	75.9	407	4 Q8N7X4	Q8N7X4 homo sapien
4	40	74.1	339	16 Q8EX24	Q8EX24 leptospira
5	40	74.1	1051	11 Q9ESV1	Q9ESV1 rattus norv
6	40	74.1	1068	11 Q8R4U7	Q8R4U7 mus musculu
7	39	72.2	267	10 Q8LSX2	Q8LSX2 chameacypar
8	39	72.2	268	10 Q8LSY0	Q8LSY0 taxodium di
9	39	72.2	268	10 Q8LSX8	Q8LSX8 sequoia sem
10	39	72.2	268	10 Q8LSY1	Q8LSY1 glyptostrob
11	39	72.2	285	10 Q8LSX5	Q8LSX5 thuja stand
12	39	72.2	285	10 Q8LSX7	Q8LSX7 chameacypar
13	39	72.2	285	10 Q8LSX6	Q8LSX6 thujopsis d
14	39	72.2	285	10 Q8LSX3	Q8LSX3 chameacypar
15	39	72.2	286	10 Q8LSX4	Q8LSX4 juniperus r
16	39	72.2	404	11 Q8R0D7	Q8R0D7 mus musculu

17	39	72.2	474	11 Q9D2C2	Q9D2C2 mus musculu
18	39	72.2	490	3 Q74804	Q74804 schizosacch
19	38	70.4	191	8 Q9XL71	Q9XL71 macaca neme
20	38	70.4	191	8 Q9XL69	Q9XL69 macaca neme
21	38	70.4	624	4 Q96N79	Q96N79 homo sapien
22	38	70.4	699	4 Q81W57	Q81W57 homo sapien
23	37	68.5	121	16 Q8EY95	Q8EY95 leptospira
24	37	68.5	321	11 Q8K0K7	Q8K0K7 mus musculu
25	37	68.5	330	11 Q8R3M2	Q8R3M2 mus musculu
26	37	68.5	334	11 Q8K2Z3	Q8K2Z3 mus musculu
27	37	68.5	895	10 Q9SD39	Q9SD39 arabidopsis
28	37	68.5	1023	4 Q9UDX0	Q9UDX0 homo sapien
29	37	68.5	1023	11 Q91WP2	Q91WP2 mus musculu
30	37	68.5	1087	3 Q9PSN9	Q9PSN9 neuropept
31	37	68.5	1555	5 Q8T1Q4	Q8T1Q4 trypanosoma
32	36	66.7	77	5 Q16935	Q16935 ancylostoma
33	36	66.7	91	5 Q16947	Q16947 ancylostoma
34	36	66.7	100	5 Q16940	Q16940 ancylostoma
35	36	66.7	223	10 Q9SSX2	Q9SSX2 barbuta ung
36	36	66.7	245	5 Q9XWP2	Q9XWP2 caenorhabdi
37	36	66.7	252	4 Q8WVK1	Q8WVK1 homo sapien
38	36	66.7	259	5 Q8T8N1	Q8T8N1 caenorhabdi
39	36	66.7	308	4 Q9P0E2	Q9P0E2 homo sapien
40	36	66.7	312	11 Q8R496	Q8R496 rattus norv
41	36	66.7	499	5 Q8MM59	Q8MM59 dirosophila
42	36	66.7	685	4 Q9UJV3	Q9UJV3 homo sapien
43	36	66.7	685	11 Q9QUS6	Q9QUS6 mus musculu
44	36	66.7	715	4 Q9UJ89	Q9UJ89 homo sapien
45	36	66.7	768	5 Q9VCR4	Q9VCR4 dirosophila

## ALIGNMENTS

## RESULT 1

Q9N8Y0 ID Q9N8Y0 PRELIMINARY; PRT; 227 AA.  
AC Q9N8Y0; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Possibly, CGI-24 protein.  
GN CHR1.101.  
OS Trypanosoma brucei.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_Taxid=5631;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=TREU927;  
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,  
RA Leonard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,  
RA Gerrard C., Rajandream M.A., Barrell B.G.,  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL929604; CAB95403.1; -  
DR InterPro; IPR006575; RMD.  
DR SMART; SM00591; RMD; 1.  
SQ SEQUENCE 227 AA; 25965 MW; DC7138488DE3F28B CRC64;

Query Match 81.5%; Score 44; DB 5; Length 227;  
Best Local Similarity 87.5%; Pred. No. 1;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ||:|||||  
DB 23 LCSEDEPPT 30

RESULT 2  
Q74378 ID Q74378 PRELIMINARY; PRT; 1009 AA.  
AC Q74378; 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE 2-oxoglutarate dehydrogenase e1 component.  
 GN SPBC3H7.03C.  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 RX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972h-;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Jimeenez Martinez J;  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL031261; CAA20299.1; -;  
 DR GeneDB Spombe; SPBC3H7.03C; -;  
 DR InterPro: IPR001017; Dehydrogenase\_E1.  
 DR InterPro: IPR005475; Transketolase\_CR.  
 DR Pfam; PF00676; E1\_dehydrog; 1.  
 DR Pfam; PF02779; transket\_pyr; 1.  
 DR TIGRFAMs; TIGR00239; 2oxo\_ch\_E1; 1.  
 SEQUENCE 1009 AA; 114163 MW; 4CB2598CE2B5E6AB CRC64;

Query Match 77.8%; Score 42; DB 3; Length 1009;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDP 7  
 Db 792 QLCNEDP 798

RESULT 3  
 ID Q8N7X4 PRELIMINARY; PRT; 407 AA.  
 AC Q8N7X4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ40242.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 Kawal-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Magatsuma M.,  
 Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,  
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isegai T.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK097361; BAC05102.1; -;  
 DR InterPro: IPR02190; MAGE.  
 DR Pfam; PF01454; MAGE; 2.  
 DR PROSITE; PS00838; MAGE; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 407 AA; 44091 MW; D674F426131244C0 CRC64;

Query Match 75.9%; Score 41; DB 4; Length 407;  
 Best Local Similarity 75.0%; Pred. No. 7;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCNEDP 8  
 Db 346 QVCNSDP 353

RESULT 4  
 Q8EXZ4 PRELIMINARY; PRT; 339 AA.  
 ID Q8EXZ4

AC Q8EXZ4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Conserved hypothetical protein.  
 GN LB063.  
 OS Leptospira interrogans.  
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
 RX NCBI\_TaxID=173;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
 RA Ren S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE011595; AAN51622.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 339 AA; 39035 MW; A7F815C3EA23CDD9 CRC64;

Query Match 74.1%; Score 40; DB 16; Length 339;  
 Best Local Similarity 85.7%; Pred. No. 9.2;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CNEDEPT 9  
 Db 152 CNEDEPT 158

RESULT 5  
 ID Q9ESV1 PRELIMINARY; PRT; 1051 AA.  
 AC Q9ESV1;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative transcription factor LUZP.  
 GN LUZP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RC MEDLINE=96411647; PubMed=8812416;  
 RA Sun D.S., Chang A.C., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
 RA Chang N.C.;  
 RT "Identification, molecular characterization, and chromosomal  
 localization of the cDNA encoding a novel leucine zipper motif-  
 containing protein."  
 RL Genomics 36:54-62(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Sun D.S., Chang A.C., Lai S.H., Hsu C.Y., Chang N.C.;  
 RT "Expression of a novel leucine zipper motif-containing protein (LUZP)  
 in brain."  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF181259; AAG02142.1; -;  
 DR HSSP; P04268; 1IC2.  
 SQ SEQUENCE 1051 AA; 117175 MW; FE1F3D7100326843 CRC64;

Query Match 74.1%; Score 40; DB 11; Length 1051;  
 Best Local Similarity 85.7%; Pred. No. 29;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPT 9  
 Db 933 CSEDEPT 939

RESULT 6  
 Q8RAU7 PRELIMINARY; PRT; 1068 AA.  
 ID Q8RAU7



AC Q8R4U7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE leucine zipper motif-containing protein.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ;  
 RX MEDLINE=96411647; PubMed=8812416;  
 RA Sun D.S., Chang A.C., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
 RA Chang N.C.;  
 RT "Identification, molecular characterization, and chromosomal  
 localization of the cDNA encoding a novel leucine zipper motif-  
 containing protein.";  
 RT Genomics 36:54-62(1996).  
 [2]  
 SEQUENCE FROM N.A.  
 STRAIN=129/SvJ;  
 RX MEDLINE=21558455; PubMed=11702014;  
 RA Lee M.W., Chang A.C., Sun D.S., Hsu C.Y., Chang N.C.;  
 RT "Restricted Expression of LUPP in Neural Lineage Cells: A Study in  
 Embryonic Stem Cells.";  
 RT J. Biomed. Sci. 8:504-511(2001).  
 DR EMBL; AF362727; AAM00269.1; -.  
 DR HSSP; P04268; 1IC2.  
 SQ SEQUENCE 1068 AA; 119404 MW; 148153E01C1643C3 CRC64;

Query Match 74.1%; Score 40; DB 11; Length 1068;  
 Best Local Similarity 85.7%; Pred. No. 29;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPPT 9  
 DB 928 CSEDPPT 934

RESULT 7  
 Q8LSX2 PRELIMINARY; PRT; 267 AA.  
 ID Q8LSX2;  
 AC Q8LSX2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myb transcription factor (Fragment).  
 OS Chaamecypris pisifera.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;  
 OC Chaamecypris.  
 OX NCBI\_TaxID=99808;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21959336; PubMed=11961107;  
 RA Kusumi J., Tsumura Y., Yoshimaru H., Tachida H.;  
 RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of  
 Conifer Trees.";  
 RT Mol. Biol. Evol. 19:736-747(2002).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.  
 DR EMBL; AB076600; BAB91464.1; -.  
 DR InterPro; IPR001005; MYB\_DNA\_binding.  
 DR Pfam; PF00249; myb\_DNA\_binding; 1.  
 DR SMART; SM00717; SANT; 1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 1.  
 KW Nuclear protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 267 AA; 28342 MW; F0FE23272A9299CA CRC64;

Query Match 72.2%; Score 39; DB 10; Length 267;  
 Best Local Similarity 75.0%; Pred. No. 11;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9  
 DB 146 LCSDPPT 153

RESULT 8  
 Q8LSY0 PRELIMINARY; PRT; 268 AA.  
 ID Q8LSY0;  
 AC Q8LSY0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myb transcription factor (Fragment).  
 OS Taxodium distichum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Taxodiaceae;  
 OX NCBI\_TaxID=28982;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21959336; PubMed=11961107;  
 RA Kusumi J., Tsumura Y., Yoshimaru H., Tachida H.;  
 RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of  
 Conifer Trees.";  
 RT Mol. Biol. Evol. 19:736-747(2002).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.  
 DR EMBL; AB076592; BAB91456.1; -.  
 DR InterPro; IPR001005; MYB\_DNA\_binding.  
 DR Pfam; PF00249; myb\_DNA\_binding; 1.  
 DR SMART; SM00717; SANT; 1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 1.  
 KW Nuclear protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 268 AA; 28545 MW; 0A17853E70424FA5 CRC64;

Query Match 72.2%; Score 39; DB 10; Length 268;  
 Best Local Similarity 75.0%; Pred. No. 11;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9  
 DB 146 LCSDPPT 153

RESULT 9  
 Q8LSX8 PRELIMINARY; PRT; 268 AA.  
 ID Q8LSX8;  
 AC Q8LSX8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myb transcription factor (Fragment).  
 OS Sequoia sempervirens (California redwood).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Sequoia.  
 OX NCBI\_TaxID=28980;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21959336; PubMed=11961107;  
 RA Kusumi J., Tsumura Y., Yoshimaru H., Tachida H.;  
 RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of  
 Conifer Trees.";  
 RT Mol. Biol. Evol. 19:736-747(2002).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.  
 DR EMBL; AB076594; BAB91458.1; -.

DR InterPro; IPR001005; MYB DNA binding.  
DR Pfam; PF00249; myb DNA-binding; 1.  
DR SMART; SM00717; SANT; 1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS50090; MYB\_3; 1.  
KW Nuclear protein.  
FT NON\_TER 1  
SQ SEQUENCE 268 AA; 28727 MW; 98CF7F872A24031B CRC64;

Query Match 72.2%; Score 39; DB 10; Length 268;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
||:||||  
Db 146 LCSSDPPT 153

## RESULT 10

Q8LSY1 PRELIMINARY; PRT; 268 AA.

DT 01-OCT-2002 (TRENBLREL. 22, Created)  
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE MYB transcription factor (Fragment).  
GN MYB.

OS Glyptostrobilus lineatus.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;  
OC Glyptostrobilus.  
OX NCBI\_TaxID=28978;  
[1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=21959336; PubMed=11961107;  
RA Kusum J., Tsunura Y., Yoshimaru H., Tachida H.;  
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of  
RT Conifer Trees."  
RL Mol. Biol. Evol. 19:736-747(2002).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

DR EMBL; AB076591; BAB91455.1; -  
DR InterPro; IPR001005; MYB DNA-binding.  
DR Pfam; PF00249; myb DNA-binding; 1.  
DR SMART; SM00717; SANT; 1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS50090; MYB\_3; 1.  
KW Nuclear protein.  
FT NON\_TER 1  
SQ SEQUENCE 268 AA; 28597 MW; D196D2C3126A5ECF CRC64;

Query Match 72.2%; Score 39; DB 10; Length 268;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
||:||||  
Db 146 LCSSDPPT 153

## RESULT 11

Q8LSX5 PRELIMINARY; PRT; 285 AA.

DT 01-OCT-2002 (TRENBLREL. 22, Created)  
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE MYB transcription factor (Fragment).  
GN MYB.

OS Thruja standishii.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thruja.  
OX NCBI\_TaxID=89194;

RN [1]  
SEQUENCE FROM N.A.

RP MEDLINE=21959336; PubMed=11961107;  
RA Kusum J., Tsunura Y., Yoshimaru H., Tachida H.;  
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of  
RT Conifer Trees."  
RL Mol. Biol. Evol. 19:736-747(2002).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

DR EMBL; AB076597; BAB91461.1; -  
DR InterPro; IPR001005; MYB DNA-binding.  
DR Pfam; PF00249; myb DNA-binding; 1.  
DR SMART; SM00717; SANT; 1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS50090; MYB\_3; 1.  
KW Nuclear protein.  
FT NON\_TER 1  
SQ SEQUENCE 285 AA; 30436 MW; CCDAB13A5A052725 CRC64;

Query Match 72.2%; Score 39; DB 10; Length 285;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
||:||||  
Db 163 LCSSDPPT 170

## RESULT 12

Q8LSX7 PRELIMINARY; PRT; 285 AA.

DT 01-OCT-2002 (TRENBLREL. 22, Created)  
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE MYB transcription factor (Fragment).  
GN MYB.

OS Chamaecyparis pisifera.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;  
OC Chamaecyparis.  
OX NCBI\_TaxID=99808;  
[1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=21959336; PubMed=11961107;  
RA Kusum J., Tsunura Y., Yoshimaru H., Tachida H.;  
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of  
RT Conifer Trees."  
RL Mol. Biol. Evol. 19:736-747(2002).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

DR EMBL; AB076595; BAB91459.1; -  
DR InterPro; IPR001005; MYB DNA-binding.  
DR Pfam; PF00249; myb DNA-binding; 1.  
DR SMART; SM00717; SANT; 1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS50090; MYB\_3; 1.  
KW Nuclear protein.  
FT NON\_TER 1  
SQ SEQUENCE 285 AA; 30272 MW; D1039F7FF610ADDF CRC64;

Query Match 72.2%; Score 39; DB 10; Length 285;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
||:||||  
Db 163 LCSSDPPT 170

## RESULT 13

Q8LSX6 PRELIMINARY; PRT; 285 AA.

```
AC Q8LSX6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.
OS Thujopsis dolabrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thujopsis.
OX NCB1_TaxID=13727;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsumura Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB076596; BAB91460.1; -
InterPro: IPR001005; Myb DNA binding.
Pfam: PF00249; myb DNA-binding; 1.
DR SMART: SM00717; SANT; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 285 AA; 30429 MW; F875D9C8EF2402F3 CRC64;

Query Match
Best Local Similarity 72.2%; Score 39; DB 10; Length 285;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
DB 163 LCSSDPPT 170

RESULT 14
Q8LSX3 PRELIMINARY; PRT; 285 AA.
AC Q8LSX3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.
OS Chamaecyparis obtusa (Japanese Cypress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
OC Chamaecyparis.
OX NCB1_TaxID=13415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsumura Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB076599; BAB91463.1; -
InterPro: IPR001005; Myb DNA binding.
Pfam: PF00249; myb DNA-binding; 1.
DR SMART: SM00717; SANT; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 285 AA; 30290 MW; 876C964CA0A3A7108 CRC64;

Query Match
Best Local Similarity 72.2%; Score 39; DB 10; Length 285;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
DB 163 LCSSDPPT 170

RESULT 15
Q8LSX4 PRELIMINARY; PRT; 286 AA.
AC Q8LSX4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.
OS Juniperus rigida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCB1_TaxID=99809;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsumura Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB076598; BAB91462.1; -
InterPro: IPR001005; Myb DNA binding.
Pfam: PF00249; myb DNA-binding; 1.
DR SMART: SM00717; SANT; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 286 AA; 30647 MW; 7582049879D40A22 CRC64;

Query Match
Best Local Similarity 72.2%; Score 39; DB 10; Length 286;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
DB 164 LCSSDPPT 171
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Search completed: September 10, 2003, 17:42:05  
Job time : 27.2 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:34:47 ; Search time 9 Seconds  
(without alignments)  
47.027 Million cell updates/sec

Title: US-09-759-112a-36  
Perfect score: 54  
Sequence: 1 QLCNEDPPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	72.2	399	1 TE21_HUMAN	Q9nyb0 homo sapien
2	38	70.4	272	1 IL2A_HUMAN	P01589 homo sapien
3	37	68.5	701	1 YAB5_SCHPO	009807 schizosacch
4	37	68.5	1002	1 ODO1_HUMAN	002218 homo sapien
5	36	66.7	268	1 IL2A_CANFA	061690 canis fami
6	36	66.7	275	1 IL2A_FELCA	P41690 felis silve
7	36	66.7	359	1 TP5B_CABEL	Q20351 caenorhabdi
8	36	66.7	385	1 TP5T_DROME	Q9vub7 drosophila
9	35	64.8	380	1 TP5A_CABEL	077081 caenorhabdi
10	35	64.8	393	1 TE21_MOUSE	091418 mus musculu
11	35	64.8	491	1 KCS3_RABIT	091c17 oryctolagus
12	35	64.8	598	1 KCS3_RAT	088759 rattus norv
13	35	64.8	598	1 GATE_TREVO	Q97919 thermoplas
14	35	64.8	692	1 DPB2_YEAST	P24482 saccharomyc
15	35	64.8	1420	1 SRB3_YEAST	P38931 saccharomyc
16	34	63.0	275	1 IL2A_BOVIN	P12342 bos taurus
17	34	63.0	275	1 IL2A_SHEEP	P26898 ovie aries
18	34	63.0	322	1 SSAR_SALTY	F74860 salmonella
19	34	63.0	340	1 TP5B_SCHPO	013749 schizosacch
20	34	63.0	376	1 TP52_MOUSE	088856 mus musculu
21	34	63.0	377	1 TP52_HUMAN	060704 homo sapien
22	34	63.0	621	1 GP63_LEIGU	000689 leishmania
23	34	63.0	860	1 CH12_COCPO	P54197 coccidioid
24	34	63.0	1003	1 TP3A_MOUSE	070157 mus musculu
25	34	63.0	1928	1 LPH_RAT	Q02401 rattus norv
26	33	61.1	168	1 PR1A_TOBAC	P08289 nicotiana t
27	33	61.1	168	1 PR1B_TOBAC	P07053 nicotiana t
28	33	61.1	168	1 PR1C_TOBAC	P09042 nicotiana t
29	33	61.1	173	1 PR1_MEDPR	Q40374 medicago tr
30	33	61.1	175	1 PR1A_LYCRES	008697 lycopersico
31	33	61.1	177	1 PR1B_TOBAC	P11670 nicotiana t
32	33	61.1	201	1 RHL1_PSEAE	P54291 pseudomonas
33	33	61.1	210	1 INSR_MACMU	Q28516 macaca mula

34	33	61.1	211	1	NDK5_MOUSE	Q99mh5 mus musculu
35	33	61.1	256	1	TP51_BRARE	Q9pce6 brycondanio
36	33	61.1	324	1	SG10_CABEL	P46568 caenorhabdi
37	33	61.1	370	1	TP51_HUMAN	060507 homo sapien
38	33	61.1	370	1	TP51_MOUSE	070281 mus musculu
39	33	61.1	611	1	GHR_COLLI	Q90375 columba liv
40	33	61.1	731	1	HRPM_PSESEY	P20401 pseudomonas
41	33	61.1	816	1	NP42_MOUSE	P97460 mus musculu
42	33	61.1	1001	1	TP3A_HUMAN	Q13472 homo sapien
43	33	61.1	1014	1	OD01_YEAST	P20967 saccharomyc
44	33	61.1	1372	1	INSR_MOUSE	P15208 mus musculu
45	33	61.1	1382	1	INSR_HUMAN	P06213 homo sapien

ALIGNMENTS

RESULT 1  
TE21\_HUMAN STANDARD; PRT; 399 AA.  
ID AC Q9NYE0; Q8WYZ3; Q9NMR2;  
DT 28-FEB-2003 (rel. 41, Created)  
DT 28-FEB-2003 (rel. 41, Last sequence update)  
DT 15-SEP-2003 (rel. 42, Last annotation update)  
DE Telomeric repeat binding factor 2 interacting protein 1 (TRF2-  
DE interacting telomeric protein Rapi) (hrapi).  
GN TRF2IP OR RAPI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=20306663; PubMed=10850490;  
RA Li B., Oestreich S., de Lange T.;  
RT "Identification of human RAPI: Implications for telomere evolution.";  
RN Cell 101:471-483(2000).  
[2]  
RP SEQUENCE FROM N.A.  
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,  
RA Wan D.F., Gu J.R.;  
RT "Novel human CDNA clones with function of inhibiting cancer cell  
RT growth.";  
RN Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ileal mucosa;  
RA Tansgami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,  
RA Hiro M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,  
RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;  
RT "NEO human cDNA sequencing project.";  
RN Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
[4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung, and Skin;  
RX MEDLINE=22386257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grove L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stalderon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.T., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,  
RA Raha S.S., Loquejano N.A., Peters G.J., Abramson R.D., Mullany P.H.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Richardson D.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RX STRUCTURE OF 132-190 BY NMR.  
 RA MEDLINE=21431821; PubMed=11545594;  
 RA Hanaka S., Nagado A., Yoshimura S., Almoto S., Li B., de Lange T.,  
 RA Nishimura Y.;  
 RT "NMR structure of the hRap1 Myb motif reveals a canonical three-helix  
 RT bundle lacking the positive surface charge typical of Myb DNA-binding  
 RT domains."  
 RL J. Mol. Biol. 312:167-175(2001).  
 CC -1- FUNCTION: May play a role in telomere length regulation.  
 CC -1- SUBUNIT: Homodimer. Binds to TRF2 (but not TRF1) with its  
 CC C-terminus.  
 CC -1- SUBCELLULAR LOCATION: Nuclear. Colocalizes with telomeric DNA in  
 CC Interphase and metaphase cells.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous; highly expressed.  
 CC -1- MISCELLANEOUS: Recruited to telomeres by TRF2; seemingly it does  
 CC not directly bind to DNA itself.  
 CC -1- SIMILARITY: Contains 1 BRCT domain.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a  
 CC frameshift in position 151.  
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a  
 CC stop codon in position 299.  
 CC -----  
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DR EMBL; AF262988; AAF72711.1; -  
 DR EMBL; AF289599; AAL5783.1; ALT\_FRAME.  
 DR EMBL; AK000669; BAA91317.1; ALT\_TERM.  
 DR EMBL; BC004465; AAH04465.1; -  
 DR EMBL; BC005841; AAH05841.1; -  
 DR EMBL; BC022428; AAH22428.1; -  
 DR PDB; 1FEK; 19-SEP-01.  
 DR Genew; HGNC:19246; TRF2IP.  
 DR MIM; 605061; -  
 DR GO; GO:0000228; C:nuclear chromosome; TAS.  
 DR GO; GO:0007004; P:telomerase-dependent telomere maintenance; TAS.  
 DR GO; GO:0007003; P:telomere binding; TAS.  
 DR InterPro; IPR001357; BRCT.  
 DR InterPro; IPR001005; Myb DNA binding.  
 DR PROSITE; PS50172; BRCT; FALSE NEG.  
 DR PROSITE; PS50090; MYB\_3; FALSE NEG.  
 DR Nuclear protein; Chromosomal protein; Telomere; 3D-structure.  
 FT DOMAIN 78 101 BRCT.  
 FT DNA\_BIND 128 188 MYB.  
 FT DOMAIN 214 304 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 383 399 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT CONFLICT 83 83 Y -> H (IN REF. 3).  
 SQ SEQUENCE 399 AA; 44260 MM; EAA615777F9D3DD CRC64;

Query Match 72.2%; Score 39; DB 1; Length 399;  
 Best Local Similarity 62.5%; Pred. No. 7;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
 DB 279 MCDDDPPT 286

RESULT 2  
 IL2A\_HUMAN STANDARD, PRT, 272 AA.  
 IL2A\_HUMAN  
 AC P01589;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha  
 DE subunit) (P55) (TAC antigen) (CD25 antigen).  
 GN IL2RA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85012734; PubMed=6090949;  
 RA Nikaide T., Shimizu A., Ishida N., Sabe H., Teshigawara K., Maeda M.,  
 RA Uchiyama T., Yodoi J., Honjo T.;  
 RT "Molecular cloning of cDNA encoding human interleukin-2 receptor."  
 RL Nature 311:631-635(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85012733; PubMed=6090948;  
 RA Leonard W.J., Depper J.M., Crabtree G.R., Rudikoff S., Pumphrey J.,  
 RA Robb R.J., Krenke M., Svetlik P.B., Peffer N.J., Waldmann T.A.,  
 RA Greene W.C.;  
 RT "Molecular cloning and expression of cDNAs for the human  
 RT interleukin-2 receptor."  
 RL Nature 311:626-631(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86067183; PubMed=2999698;  
 RA Ishida N., Kanamori H., Noma T., Nikaide T., Sabe H., Suzuki N.,  
 RA Shimizu A., Honjo T.;  
 RT "Molecular cloning and structure of the human interleukin 2 receptor  
 RT gene."  
 RL Nucleic Acids Res. 13:7579-7589(1985).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86018688; PubMed=2996141;  
 RA Leonard W.J., Depper J.M., Kanahisa M., Krenke M., Peffer N.J.,  
 RA Svetlik P.B., Sullivan W., Greene W.C.;  
 RT "Structure of the human interleukin-2 receptor gene."  
 RL Science 230:633-639(1985).  
 RN [5]  
 RP SEQUENCE OF 1-21 FROM N.A.  
 RX MEDLINE=87159546; PubMed=3030566;  
 RA Cross S.L., Feinberg M.B., Wolf J.B., Holbrook N.J., Wong-Stall F.,  
 RA Leonard W.J.;  
 RT "Regulation of the human interleukin-2 receptor alpha chain promoter:  
 RT activation of a nonfunctional promoter by the transactivator gene of  
 RT HTLV-I."  
 RL Cell 49:47-56(1987).  
 RN [6]  
 RP 3D-STRUCTURE MODELING OF 23-83.  
 RX MEDLINE=95111955; PubMed=7529123;  
 RA Bamborough P., Hedgecock C.J., Richards W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 RT modeling."  
 RL Structure 2:839-851(1994).  
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.  
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R  
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE  
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA  
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE  
 CC WITH A GAMMA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD25 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd25.htm".  
 CC -----  
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CC -----
DR EMBL; X01057; CAA25525.1; -
DR EMBL; X01131; CAA26906.1; -
DR EMBL; X01132; CAA26906.1; JOINED.
DR EMBL; X01133; CAA26906.1; JOINED.
DR EMBL; X01134; CAA26906.1; JOINED.
DR EMBL; X01135; CAA26906.1; JOINED.
DR EMBL; X01136; CAA26906.1; JOINED.
DR EMBL; X01137; CAA26906.1; JOINED.
DR EMBL; X01138; CAA26906.1; JOINED.
DR EMBL; X01122; AAB59535.1; ALT_SEQ.
DR EMBL; X01066; AAA67527.1; -
DR EMBL; M10322; AAA67527.1; JOINED.
DR EMBL; M1060; AAA67527.1; JOINED.
DR EMBL; M1061; AAA67527.1; JOINED.
DR EMBL; M1062; AAA67527.1; JOINED.
DR EMBL; M1063; AAA67527.1; JOINED.
DR EMBL; M1064; AAA67527.1; JOINED.
DR EMBL; M1065; AAA67527.1; JOINED.
DR EMBL; M15864; AAA59162.1; -
DR PIR; A44186; UNH02.
DR PDB; 11LM; 26-JAN-95.
DR PDB; 11LN; 26-JAN-95.
DR Genew; HGNC; 6008; IL2RA.
DR MIM; 14730; -
DR MIM; 606367; -
DR GO; GO:0005886; Cytoplasm membrane; TAS.
DR GO; GO:0004911; F-interleukin-2 receptor activity; TAS.
DR GO; GO:0008915; P:apoptosis; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPRO00436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
DR KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi; 3d-structure.
FT SIGNAL 1 21
FT CHAIN 22 272 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 259 POTENTIAL.
FT DOMAIN 260 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 81 SUSHI 1.
FT DOMAIN 124 185 SUSHI 2.
FT DISULFID 24 67 BY SIMILARITY.
FT DISULFID 751 80 BY SIMILARITY.
FT DISULFID 125 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT STRAND 35 36
FT TURN 43 44
FT STRAND 46 50
FT STRAND 64 67
FT STRAND 70 70
FT TURN 71 72
FT STRAND 73 73
FT STRAND 76 76
SQ SEQUENCE 272 AA; 30819 MW; 83D907C8C81D2C0E CRC64;

Query Match 70.4%; Score 38; DB 1; Length 272;
Best Local Similarity 62.5%; Pred. No. 7;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QLCNEDPP 8  
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Db 22 ELCDDDP 29

RESULT 3  
YABS\_SCHPO

```

ID YABS_SCHPO STANDARD; PRT; 701 AA.
AC 009807;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C2G11.05c in chromosome I.
GN SPAC2G11.05c.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolcraet G., Aert R., Robben J., Grynopre B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambut R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garcon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cernutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
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DR EMBL; Z54354; CAA91170.1; -

DR PIR; T38571; S62460.

DR Genedb; SPombe; SPAC2G11.05c; -

DR InterPro; IPRO04328; BRO1.

DR Pfam; PF03097; BRO1; 1.

KW Hypothetical protein

SQ SEQUENCE 701 AA; 81769 MW; E13B4C4AE085671 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 701;  
Best Local Similarity 85.7%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPP 8  
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Db 122 LCNEDPP 128

RESULT 4  
ID ODO1\_HUMAN STANDARD; PRT; 1002 AA.  
ID ODO1\_HUMAN  
AC 002218;  
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor  
DE (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase).  
GN OGDH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=92179301; PubMed=1542694;  
RA Koike K., Umeta Y., Goto S.;  
RT "Cloning and nucleotide sequence of the cDNA encoding human 2-oxoglutarate dehydrogenase (lipoamide).";  
RT Proc. Natl. Acad. Sci. U.S.A. 89:1963-1967(1992).  
RN [2]  
RP REVISIONS, SEQUENCE FROM N.A.  
RP MEDLINE=95347609; PubMed=7622061;  
KOIKE K.;  
"The gene encoding human 2-oxoglutarate dehydrogenase: structural organization and mapping to chromosome 7p13-p14.";  
Gene 159:261-266(1995).  
CC -1- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF 3 ENZYMATIC COMPONENTS: 2-OXOGLUTARATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E3).  
CC -1- CATALYTIC ACTIVITY: 2-oxoglutarate + lipoamide = S-succinyl-dihydrolipoamide + CO(2).  
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.  
CC -1- ENZYME REGULATION: CATABOLITE REPPRESSED.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -----  
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CC -----  
DR EMBL; D10523; BAA01393.1; -;  
DR EMBL; D32064; BAA06836.1; -;  
DR EMBL; D32056; BAA06836.1; JOINED.  
DR EMBL; D32057; BAA06836.1; JOINED.  
DR EMBL; D32058; BAA06836.1; JOINED.  
DR EMBL; D32059; BAA06836.1; JOINED.  
DR EMBL; D32060; BAA06836.1; JOINED.  
DR EMBL; D32061; BAA06836.1; JOINED.  
DR EMBL; D32062; BAA06836.1; JOINED.  
DR EMBL; D32063; BAA06836.1; JOINED.  
DR Genew; HGNC:8124; OGDH.  
DR GK; Q02218; -;  
DR MIM; 203740; -;  
DR GO; GO:0006091; P:energy pathway; TAS.  
DR InterPro; IPR001017; Dehydrogenase\_E1.  
DR InterPro; IPR005475; Transketolase\_CR.  
DR Pfam; PF00676; E1 dehydrog; 1.  
DR TrEMBL; TIGR00239; 2oxo dh E1; 1.  
KM Glycerol-3-phosphate: Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;  
KM Mitochondrion; Transit peptide;  
FT TRANSIT 1  
FT CHAIN 41 1002  
FT 2-OXOGLUTARATE DEHYDROGENASE E1  
FT COMPONENT.  
FT N -> D (IN REF. 2; BAA06836).  
SQ SEQUENCE 1002 AA; 113475 MW; 28DAEFC55AC6F763 CRC64;  
Query Match 60.5%; Score 37; DB 1; Length 1002;  
Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNDDP 7  
Db 800 QMCNDP 806  
RESULT 5  
ID IL2A CANFA STANDARD; PRT; 268 AA.  
AC 062802;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).  
GN IL2RA.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Dickerson E.B., Padilla M.L., Helfand S.C.;  
RT "Cloning of the canine IL-2 receptor alpha subunit.";  
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.  
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.  
CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.  
CC -----  
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CC -----  
DR EMBL; AF056491; AAC13560.1; -;  
DR HSSP; P01589; IILM.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00084; sushi; 2.  
DR SMART; SM00032; CCP; 2.  
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.  
FT SIGNAL 1 21  
FT CHAIN 22 268  
FT DOMAIN 22 237  
FT TRANSMEM 238 258  
FT DOMAIN 259 268  
FT DOMAIN 273 282  
FT DOMAIN 121 182  
FT DISULFID 24 64  
FT DISULFID 751 77  
FT DISULFID 122 165  
FT DISULFID 149 181  
FT CARBOHYD 67 67  
SQ SEQUENCE 268 AA; 30356 MW; 6622E154FDE2E46 CRC64;  
Query Match 66.7%; Score 36; DB 1; Length 268;  
Best Local Similarity 71.4%; Pred. No. 16;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
RESULT 6  
ID IL2A\_FELCA



ID IL2A\_FELCA STANDARD; PRT; 275 AA.  
 AC P41690;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).  
 GN IL2RA.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 NCBI\_TaxId=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Matsumoto Y., Ohno K., Gotsuka R., Hirota Y., Teujimoto H., Hasegawa A.;  
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.  
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.  
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 CC -----  
 DR EMBL: D16143; BAA03714.1; -  
 DR HSSP: P01589; IILM.  
 DR InterPro: IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam: PF00084; Sushi; 2.  
 DR SMART: SM00032; CCP; 2.  
 DR Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 244 262 POTENTIAL.  
 FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 23 78 SUSHI 1.  
 FT DOMAIN 122 185 SUSHI 2.  
 FT DISULFID 24 67 BY SIMILARITY.  
 FT DISULFID 751 80 BY SIMILARITY.  
 FT DISULFID 125 164 BY SIMILARITY.  
 FT DISULFID 152 184 BY SIMILARITY.  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 70 70 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 275 AA; 30817 MW; C978BD8D06332326 CRC64;  
 Query Match 66.7%; Score 36; DB 1; Length 275;  
 Best Local Similarity 62.5%; Pred. No. 17;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QLCNEDPT 8  
 DB 22 ELCDENMP 29  
 RESULT 7  
 TPST CAEBL STANDARD; PRT; 359 AA.  
 AC Q20351;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Putative protein-tyrosine sulfotransferase (EC 2.8.2.20)  
 DE (Tyrosylprotein sulfotransferase) (TPST).

GN F42G9.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Peloderae; Caenorhabditis.  
 NCBI\_TaxId=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Bristol N2.  
 RA Taich A.;  
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE O-SULFURATION OF TYROSINE RESIDUES WITHIN ACIDIC MOTIFS OF POLYPEPTIDES (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine = adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.  
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 CC -----  
 DR EMBL: U00051; AAA91354.1; -  
 DR PIR: T16350; T16350.  
 DR WormPeP: F42G9.8; CE07235.  
 DR InterPro: IPR000863; Sulfotransferase.  
 DR Pfam: PF00685; Sulfotransfer; 1.  
 DR Hypothetical protein; Transferase; Transmembrane; Glycoprotein;  
 KM Signal-anchor.  
 FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 28 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 49 359 LUMENAL, CATALYTIC (POTENTIAL).  
 SQ SEQUENCE 359 AA; 41469 MW; 9FC2F44539B8CC53 CRC64;  
 Query Match 66.7%; Score 36; DB 1; Length 359;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QLCNEDPT 9  
 DB 166 RLCNKPPT 174  
 RESULT 8  
 TPST DROME STANDARD; PRT; 385 AA.  
 AC Q9VYE7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable protein-tyrosine sulfotransferase (EC 2.8.2.20)  
 DE (Tyrosylprotein sulfotransferase) (TPST).  
 GN CG32632/CG1573.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Gelinkler S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abriil J.F., Agbayan A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Butts K.C., Buam D.A., Butler H., Cadieu E., Cente A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Fiedler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Gloder A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Markulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mohnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Styrekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gbhe R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES WITHIN  
 CC ACIDIC MOTIFS OF POLYPEPTIDES (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine =  
 CC adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.  
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 CC  
 CC EMBL: AE003493; AAF48286.1; -  
 CC FlyBase: FBgn0052632; CG32632.  
 CC InterPro: IPR000863; Sulfotransferase.  
 CC Pfam: PF00685; Sulfotransfer; 1.  
 CC DR Hypothetical protein; transferase; Transmembrane; Glycoprotein;  
 CC KW Signal-anchor.  
 CC FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC FT (POTENTIAL).  
 CC FT DOMAIN 31 385 LUMENAL, CATALYTIC (POTENTIAL).  
 CC FT DOMAIN 362 370 POLY-ALA.  
 CC SQ SEQUENCE 385 AA; 44054 MW; 35BAE2B3E2D2FE1C CRC64;  
 CC  
 CC Query Match 66.7%; Score 36; DB 1; Length 385;  
 CC Best Local Similarity 66.7%; Pred. No. 24;  
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

AC 077081; Q9NEM9;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein-tyrosine sulfotransferase A (EC 2.8.2.20) (Tyrosylprotein  
 DE sulfotransferase-A) (TPST-A).  
 OS Y11B2A.15.  
 GN Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
 OC Rhabditidae; Ploloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 OK  
 RN  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-Bristol N2;  
 RX MEDLINE=98406128; PubMed=9733778;  
 RA Ouyang Y.-B., Moore K.L.;  
 RT "Molecular cloning and expression of human and mouse tyrosylprotein  
 RT sulfotransferase-2 and a tyrosylprotein sulfotransferase homologue in  
 RT *Caenorhabditis elegans*."  
 RL J. Biol. Chem. 273:24770-24774(1998).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Sulston J.E.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]-  
 RP REVISIONS.  
 RA Durbin R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES WITHIN  
 CC ACIDIC MOTIFS OF POLYPEPTIDES.  
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine =  
 CC adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.  
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 CC  
 CC EMBL: AF049709; AAC36062.1; -  
 CC DR EMBL: AL132804; CAC35844.1; -  
 CC DR PIR: T42755; T42755.  
 CC DR WormPep: Y11B2A.15; CE26632.  
 CC DR InterPro: IPR000863; Sulfotransferase.  
 CC Pfam: PF00685; Sulfotransfer; 1.  
 CC KW Transferase; Transmembrane; Glycoprotein; Signal-anchor.  
 CC FT DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 7 27 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC FT (POTENTIAL).  
 CC FT DOMAIN 28 380 LUMENAL, CATALYTIC (POTENTIAL).  
 CC FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC SQ SEQUENCE 380 AA; 43313 MW; FF709BF00F1EDC95 CRC64;  
 CC  
 CC Query Match 64.8%; Score 35; DB 1; Length 380;  
 CC Best Local Similarity 66.7%; Pred. No. 36;  
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLCNEDPPT 9  
 Db 156 RLCKNDPPT 164

RESULT 10  
 TE21\_MOUSE  
 ID TE21\_MOUSE STANDARD; PRT; 393 AA.  
 AC Q91VH8; Q9JUE8; Q9JUE9;  
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-FEB-2003 (Rel. 42, Last annotation update)  
 DE Telomeric repeat binding factor 2 interacting protein 1 (TRF2-  
 \*DE Interacting telomeric protein Rapi).  
 GN TRF2IP OR RAPI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L.H., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Cassavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE OF 1-280 FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,  
 RA Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library  
 made by oligo-capping method.";  
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: May play a role in telomere length regulation.  
 CC -1- SUBUNIT: Homodimer. Binds to TRF2 (but not TRF1) with its  
 CC C-terminus (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear. Colocalizes with telomeric DNA in  
 CC interphase and metaphase cells (By similarity).  
 CC -1- MISCELLANEOUS: Recruited to telomeres by TRF2; seemingly it does  
 CC not directly bind to DNA itself (By similarity).  
 CC -1- SIMILARITY: Contains 1 BRCT domain.  
 CC -1- SIMILARITY: Contains 1 Myb-like domain.  
 CC -----  
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 CC -----  
 CC EMBL, BC012270, AAH12270.1, -;  
 DR EMBL, BC017641, AAH17641.1, -;  
 DR EMBL, AB041557, BAA95042.1, -;  
 DR EMBL, AB041559, BAA95043.1, ALT\_INIT.  
 DR MGD: MGI:1929871; Tef2ip.  
 DR InterPro: IPR001357; BRCT.  
 DR InterPro: IPR001005; Myb-DNA-binding.  
 DR PROSITE: PS50172; BRCT; FALSE NEG.  
 DR PROSITE: PS50090; MYB\_3; FALSE NEG.  
 KW Nuclear protein; Chromosomal protein; Telomere.  
 FT DOMAIN 78 101 BRCT.  
 FT DNA\_BIND 125 185 MYB.  
 FT DOMAIN 232 297 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 377 393 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT CONFLICT 281 286 PTPBED -> HTHTOS (IN REF. 2).  
 SQ SEQUENCE 393 AA; 43353 MW; 7A15CFD83733BE2D CRC64;  
 Query Match  
 Best Local Similarity 64.8%; Score 35; DB 1; Length 393;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LCNEDPPT 9  
 :|||  
 Db 275 MCDGDPPT 282  
 RESULT 11  
 KC33 RABIT STANDARD; PRT; 491 AA.  
 ID KC33 RABIT  
 AC 09T17;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Potassium voltage-gated channel subfamily S member 3 (Potassium  
 DE channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).  
 GN KCN3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand white; TISSUE=Corneal epithelium;  
 RA Rae U.L.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Potassium channel subunit. Modulates channel activity  
 CC and reduces the ion flow (By similarity).  
 CC -1- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form  
 CC homomultimers. Might also bind to other channel proteins (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the  
 CC plasma membrane but remain in an intracellular compartment in the  
 CC absence of KCNB1 (By similarity).  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, AF209723, AAF22833.1, -;  
 DR InterPro: IPR000210; BTB\_POZ.  
 DR InterPro: IPR005821; Ion\_trans.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR003091; K\_channel.  
 DR InterPro: IPR003111; K\_tetra.  
 DR InterPro: IPR003971; Kv9\_channel.  
 DR InterPro: IPR003968; Kv\_channel.  
 DR InterPro: IPR005820; M+channel\_nlg.  
 DR Pfam: PF00520; ion\_trans\_1.  
 DR Pfam: PF02214; K\_tetra\_1.  
 DR PRINTS: PR00169; KCHANNEL.  
 DR PRINTS: PR01494; KV9CHANNEL.  
 DR PRINTS: PR01491; KVCHANNEL.  
 DR SMART: SM00225; BTB; 1.  
 DR Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
 KW Multigene family.  
 FT DOMAIN 1 185 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 186 206 SEGMENT S1 (POTENTIAL).  
 FT TRANSMEM 224 244 SEGMENT S2 (POTENTIAL).

FT DOMAIN 245 253 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 254 274 SEGMENT S3 (POTENTIAL).  
 FT TRANSMEM 288 308 SEGMENT S4 (POTENTIAL).  
 FT DOMAIN 309 323 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 324 344 SEGMENT S5 (POTENTIAL).  
 FT DOMAIN 358 378 SEGMENT H5 (POT-FORMING) (POTENTIAL).  
 FT TRANSMEM 386 406 SEGMENT S6 (POTENTIAL).  
 FT DOMAIN 407 491 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 491 AA; 55941 MW; 2EE396E089D6F77 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 491;  
 Best Local Similarity 83.3%; Pred. No. 48;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPP 8  
 Db 424 CSEDEPP 429

RESULT 12  
 3 RAT  
 NC KCS3 RAT STANDARD; PRT; 491 AA.  
 DT 088759; 054900; Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Potassium voltage-gated channel subfamily S member 3 (Potassium channel Kv3.3) (Delayed-rectifier K+ channel alpha subunit 3).  
 GN KCN3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_TaxID=10116;  
 (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Kidney;  
 RX MEDLINE=98031889; PubMed=9362476;  
 RA Patel A.J., Lazdunski M., Honore E.;  
 RT "Kv2.1/Kv3, a novel ATP-dependent delayed-rectifier K+ channel in oxygen-sensitive pulmonary artery myocytes";  
 RL EMBL J. 16:6615-6625(1997).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98369652; PubMed=9704029;  
 RA Stocker M., Kerscheneitner D.;  
 RT "Cloning and tissue distribution of two new potassium channel alpha-subunits cloned from rat brain";  
 DE Biochem. Biophys. Res. Commun. 248:927-934(1998).  
 -1- FUNCTION: Potassium channel subunit. Modulates channel activity and shifts the activation threshold of KCNB1 to more negative values.  
 CC -1- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form homomultimers. Might also bind to other channel proteins (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the plasma membrane but remain in an intracellular compartment in the absence of KCNB1 (By similarity).  
 CC -1- TISSUE SPECIFICITY: Detected in lung, spleen, brain and heart.  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
 CC -1- MISCELLANEOUS: Inhibited by 4-aminopyridine (4-AP). Channel activity is reversibly inhibited by hypoxia and down-regulated in the absence of intracellular ATP.  
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.  
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 CC EMBL AF029056; AAB94882.1; -  
 DR EMBL Y17607; CA176805.1; -  
 DR InterPro: IPR000210; BTB\_POZ.  
 DR InterPro: IPR005821; Ion\_trans.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR003091; K\_channel.  
 DR InterPro: IPR003131; K\_tetra.  
 DR InterPro: IPR003971; Kv3\_channel.  
 DR InterPro: IPR003968; Kv\_channel.  
 DR InterPro: IPR005820; M+channel\_nlg.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR Pfam: PF02214; K\_tetra\_1.  
 DR PRINTS: PR00169; KCHANNEL.  
 DR PRINTS: PR01494; KVCHANNEL.  
 DR PRINTS: PR01491; KVCHANNEL.  
 DR SMART: SM00225; BTB; 1.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
 KW Multigene family.  
 FT DOMAIN 1 185 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 186 206 SEGMENT S1 (POTENTIAL).  
 FT TRANSMEM 224 244 SEGMENT S2 (POTENTIAL).  
 FT DOMAIN 245 253 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 254 274 SEGMENT S3 (POTENTIAL).  
 FT TRANSMEM 288 308 SEGMENT S4 (POTENTIAL).  
 FT DOMAIN 309 323 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 324 344 SEGMENT S5 (POTENTIAL).  
 FT DOMAIN 358 378 SEGMENT H5 (POT-FORMING) (POTENTIAL).  
 FT TRANSMEM 385 405 SEGMENT S6 (POTENTIAL).  
 FT DOMAIN 406 491 CYTOPLASMIC (POTENTIAL).  
 FT CONFLICT 113 113 I -> F (IN REF. 1).  
 SQ SEQUENCE 491 AA; 55865 MW; 6157BC7FEF94CC2B CRC64;

Query Match 64.8%; Score 35; DB 1; Length 491;  
 Best Local Similarity 83.3%; Pred. No. 48;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPP 8  
 Db 424 CSEDEPP 429

RESULT 13  
 GATE\_THEVO  
 ID GATE\_THEVO STANDARD; PRT; 598 AA.  
 AC Q979L9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE GlutamyL-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-) (Glu-ADT subunit E).  
 GN GATE OR TV1141 OR TVG116951.  
 GN Archaea; Euryarchaeota; Thermoplasma; Thermoplasmales;  
 OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmales;  
 OC Thermoplasmales; Thermoplasma.  
 OK NCBI\_TaxID=50339;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GSS1 / DSM 4299 / JCM 9571;  
 RX MEDLINE=20570466; PubMed=11121031;  
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,  
 RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,  
 RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;  
 RT "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).  
 RL -1- FUNCTION: Allows the formation of correctly charged Gln-tRNA(Gln) through the transamidation of misacylated Glu-tRNA(Gln) in organisms which lack glutamyl-tRNA synthetase. The reaction takes place in the presence of glutamine and ATP through an activated gamma-phospho-Glu-tRNA(Gln). The gate system is

CC specific for glutamate and does not act on aspartate (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamyl-L-cRNA(Gln) + L-glutamine = ADP  
 CC + phosphate + L-glutaminyl-L-cRNA(Gln) + L-glutamate.  
 CC \* SUBUNIT: Heterodimer of gatl and gatl (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE GATB/GATC FAMILY. GATB SUBFAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL: AP000995; BAB60283.1; -  
 CC DR HAMAP: MF 00588; -1.  
 CC DR InterPro: IPR004413; GatlB.  
 CC DR InterPro: IPR006107; GatlB\_cent.  
 CC DR Pfam: PF01162; GatlB; 1.  
 CC Pfam: PF02934; GatlB\_N; 1.  
 CC PROSITE: PS01234; GATB; 1.  
 CC DR Protein biosynthesis; Ligase; Complete proteome.  
 CC KM SEQUENCE 598 AA; 67355 MW; 6777EB8F039F8CFC CRC64;  
 CC SQ  
 CC  
 CC Query Match 64.8%; Score 35; DB 1; Length 598;  
 CC Best Local Similarity 83.3%; Pred. No. 60;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 3 CNEDEPP 8  
 CC Db 78 CDEDDP 83  
 CC  
 CC RESULT 14  
 CC DPB2\_YEAST STANDARD; PRT; 692 AA.  
 CC AC P24482; Q06622;  
 CC DT 01-MAR-1992 (Rel. 21, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE DNA polymerase epsilon subunit B (EC 2.7.7.7) (DNA polymerase II  
 CC subunit B).  
 CC GN DPB2 OR YPR175W OR P9705.7.  
 CC OS Saccharomyces cerevisiae (Baker's Yeast).  
 CC NC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CC NCB1\_TaxID=4932;  
 CC [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=YH48.  
 CC RX MEDLINE=912121; PubMed=2052544;  
 CC RA Araki H., Hamatake R.K., Johnston L.H., Sugino A.;  
 CC RT "DPB2, the gene encoding DNA polymerase II subunit B, is required for  
 CC chromosome replication in Saccharomyces cerevisiae.";  
 CC Proc. Natl. Acad. Sci. U.S.A. 88:4601-4605(1991).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=S288c; AB972;  
 CC RX MEDLINE=9731321; PubMed=9169875;  
 CC RA Busey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansgore W.,  
 CC RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,  
 CC RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,  
 CC RA Chung E., Churcher C.M., Cosser F., Davis K., Davis R.W.,  
 CC RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesthoeft A.,  
 CC RA Duncan M., Floeth M., Fortin N., Friesen J.D., Filtz C., Goffeau A.,  
 CC RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,  
 CC RA Hunke-Smith S., Hyman R., Johnston M., Kalman S., Kline K.,  
 CC RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,  
 CC RA Marathe R., Messenguy F., Mewes H.-W., Mitterpeter S., Mostl D.,  
 CC RA Mueller-Auer S., Namach A., Nentwich U., Oefner P., Pearson D.,  
 CC RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,

RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,  
 RA Urrastarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,  
 RA Walsh S.V., Wambut R., Wang Y., Wedler E., Wedler H., Winnett E.,  
 RA Zhong W.M., Zollner A., Vo D.H., Hani J.;  
 CC "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI";  
 CC Nature 387:103-105(1997).  
 CC RL Nature 387:103-105(1997).  
 CC -1- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA  
 CC REPLICATION. DPB2 IS ESSENTIAL FOR CELL GROWTH. MAY HAVE A ROLE IN  
 CC DNA SYNTHESIS.  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 CC + [DNA] (N).  
 CC -1- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30  
 CC kDa, AND 29 kDa).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:  
 CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR  
 CC DIFFERENT REACTIONS OF DNA SYNTHESIS.  
 CC -1- SIMILARITY: TO OTHER SPECIES DNA POLYMERASE EPSILON, SUBUNIT B.  
 CC -----  
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 CC -----  
 CC DR EMBL: M61710; AAA34576.1; ALT\_INIT.  
 CC DR EMBL: U25842; AAB68109.1; -  
 CC DR PIR: S59833; S59833.  
 CC DR SGD: S0006379; DPB2.  
 CC DR Pfam: PF04042; DNA pol E B; 1.  
 CC KM Transferrase; DNA-directed DNA polymerase; DNA replication;  
 CC KM DNA-binding; Nuclear protein.  
 CC FT CONFLICT 461 461 F -> Y (IN REF. 1).  
 CC FT 524 524 K -> R (IN REF. 1).  
 CC FT CONFLICT 568 568 V -> F (IN REF. 1).  
 CC FT 587 587 E -> Q (IN REF. 1).  
 CC FT CONFLICT 647 647 T -> I (IN REF. 1).  
 CC KM SEQUENCE 692 AA; 78703 MW; 5C01647BD2B6A39A CRC64;  
 CC SQ  
 CC  
 CC Query Match 64.8%; Score 35; DB 1; Length 692;  
 CC Best Local Similarity 66.7%; Pred. No. 70;  
 CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 CC  
 CC QY 1 QLCNEDEPP 9  
 CC Db 425 QKLNDDPPT 433  
 CC  
 CC RESULT 15  
 CC SRS9\_YEAST STANDARD; PRT; 1420 AA.  
 CC ID SRS9\_YEAST  
 CC AC P38931;  
 CC DT 01-FEB-1995 (Rel. 31, Created)  
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 CC DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 CC DE Suppressor of RNA polymerase B SRS9 (SCA1 protein).  
 CC GN SRS9 OR SCA1 OR SSN2 OR YDR443C.  
 CC OS Saccharomyces cerevisiae (Baker's Yeast).  
 CC NC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CC NCB1\_TaxID=4932;  
 CC [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=S288c;  
 CC RX MEDLINE=95293223; PubMed=7774808;  
 CC RA Hengartner C.J., Thompson C.M., Zhang J., Chao D.M., Liao S.-M.,  
 CC RA Koloske A.J., Okamura S., Young R.A.;  
 CC RT "Association of an activator with an RNA polymerase II holoenzyme";  
 CC Genes Dev. 9:897-910(1995).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.

RA Yuryev A., Gorden J.L.;  
 RN Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,  
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,  
 RA Hunnicke-Smith S., Hymen R., Komp C., Lashkari D., Lew H., Lin D.,  
 RA Mosedale D., Nakahara K., Namach A., Oefner P., Oh C., Petel F.X.,  
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,  
 RA Winant A., Yelton M., Boetstein D., Davis R.W.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: COMPONENT OF THE RNA POLYMERASE II HOLOENZYME AND THE  
 CC MEDITOR OF ACTIVATION SUBCOMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).  
 CC -----  
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 CC -----  
 DR EMBL; U23812; AAA91316.1; -;  
 DR EMBL; U09176; AAA18614.1; -;  
 DR EMBL; U33007; AAB64875.1; -;  
 DR PIR; B57062; B57062.  
 DR TRASNFRAC; T02153; -;  
 DR SGD; S0002851; SSN2.  
 KW Nuclear protein.  
 FT DOMAIN 526 529 POLY-ASN.  
 FT DOMAIN 526 529 POLY-GLU.  
 FT DOMAIN 657 664 POLY-SER.  
 FT DOMAIN 813 816 POLY-LEU.  
 FT DOMAIN 1005 1008 POLY-GLN.  
 FT DOMAIN 1121 1136 POLY-GLN.  
 FT CONFLICT 38 38 D -> E (IN REF. 2).  
 FT CONFLICT 812 812 E -> V (IN REF. 2).  
 FT CONFLICT 859 859 T -> S (IN REF. 2).  
 FT CONFLICT 877 878 VK -> GE (IN REF. 2).  
 FT CONFLICT 887 887 T -> P (IN REF. 2).  
 FT CONFLICT 1284 1284 Y -> S (IN REF. 2).  
 SQ SEQUENCE 1420 AA; 160000 MW; 7F6CFABBE0FAC918 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 1420;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 QLCNEDDP 8  
 :|.|.|.|.  
 985 KLTNEDDP 992

Search completed: September 10, 2003, 17:40:53  
 Job time : 10 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:38:22 ; Search time 12.15 Seconds  
(without alignments)  
71.236 Million cell updates/sec

Title: US-09-759-112a-36

Perfect score: 54  
Sequence: 1 OLCNEDDPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Reached: 283308 seqs, 96168682 residues  
1 number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	1009	2 T40412	2-oxoglutarate dehydrogenase e1 component - fission yeast (Schizosaccharomyces pombe)
2	39	72.2	102	4 A37413	hypothetical RTVL-H3 promoter region/calbindin fusion protein - human (fragment)
3	39	72.2	490	2 T40116	hypothetical protein
4	38	70.4	272	1 UH02	interleukin-2 receptor
5	37	68.5	701	2 S62460	hypothetical protein
6	37	68.5	895	2 T45738	hypothetical protein
7	37	68.5	1003	2 A38234	oxoglutarate dehydrogenase
8	37	68.5	1022	2 T49683	probable oxoglutarate dehydrogenase
9	36	66.7	245	2 T26868	hypothetical protein
10	36	66.7	359	2 T16350	hypothetical protein
11	35	64.8	185	2 T10677	pathogenesis-related protein
12	35	64.8	283	2 C75518	strigolactone 3-kinase
13	35	64.8	334	2 T11633	hypothetical protein
14	35	64.8	380	2 T42755	tyrosylprotein sulfotransferase
15	35	64.8	491	2 U80276	voltage-gated potassium channel
16	35	64.8	692	1 B57062	DNA-directed DNA polymerase
17	35	64.8	1420	2 B57062	SRB9 protein - yeast
18	35	64.8	2055	2 T00093	hypothetical protein
19	34	63.0	275	1 JCI113	interleukin-2 receptor
20	34	63.0	322	1 S07442	interleukin-2 receptor
21	34	63.0	322	2 AB0697	probable type III proteinase
22	34	63.0	340	2 T37796	transcription factor
23	34	63.0	397	2 S20617	MDR-type permease
24	34	63.0	472	2 C97311	hypothetical protein
25	34	63.0	701	2 T37882	hypothetical protein
26	34	63.0	730	2 S48813	chitinase (EC 3.2.1.15)
27	34	63.0	860	2 J04566	hypothetical protein
28	34	63.0	962	2 T00262	hypothetical protein
29	34	63.0	1003	2 T13951	DNA topoisomerase

30	34	63.0	1928	2 J50610	beta-galactosidase
31	33	61.1	112	2 S19971	Ig kappa chain V region
32	33	61.1	131	2 PH1226	Ig kappa chain pre
33	33	61.1	161	2 E85354	PR-1-like protein
34	33	61.1	161	2 H84518	pathogenesis-related protein
35	33	61.1	161	2 T52399	pathogenesis-related protein
36	33	61.1	163	2 T04989	pathogenesis-related protein
37	33	61.1	168	2 A24620	pathogenesis-related protein
38	33	61.1	168	2 C24620	pathogenesis-related protein
39	33	61.1	168	2 B24620	pathogenesis-related protein
40	33	61.1	169	2 F87713	conserved hypothetical protein
41	33	61.1	173	2 S47171	gene PR-1 protein
42	33	61.1	174	2 S71554	pathogenesis-related protein
43	33	61.1	175	2 S43894	pathogenesis-related protein
44	33	61.1	177	2 S04728	pathogenesis-related protein
45	33	61.1	177	2 T08126	pathogenesis-related protein

## ALIGNMENTS

RESULT 1  
T40412  
2-oxoglutarate dehydrogenase e1 component - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
C:Accession: T40412  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.  
Submitted to the EMBL Data Library, August 1998  
A:Reference number: Z21926  
A:Accession: T40412  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1009 <LVN>  
A:Cross-references: EMBL:AL031261; PIDN:CAA20299.1; GSPDB:GN00067; SPDB:SPBC3H7.03c  
A:Experimental source: strain 972h-; cosmid C3H7  
C:Genetics:  
A:Gene: SPDB:SPBC3H7.03c  
A:Map position: 2  
C:Superfamily: oxoglutarate dehydrogenase (liponamide); thiamin pyrophosphate-binding domain

Query Match  
Best Local Similarity 77.8%; Score 42; DB 2; Length 1009;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OLCNEDP 7  
DB 792 OLCNEDP 798

RESULT 2  
A37413  
Hypothetical RTVL-H3 promoter region/calbindin fusion protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000  
C:Accession: A37413  
R:Liou, A.Y.; Abraham, B.A.  
Cancer Res. 51, 4107-4110, 1991  
A:Title: Subtractive cloning of a hybrid human endogenous retrovirus and calbindin gene  
A:Reference number: A37413; MUID:91309099; PMID:1713126  
A:Accession: A37413  
A:Molecule type: mRNA  
A:Residues: 1-102 <LIU>  
A:Cross-references: GB:S46006; NID:G1679976; PIDN:AB19408.1; PID:G233226  
A:Experimental source: prostate bone metastasis cell line PC3  
A:Note: sequence extracted from NCBI backbone (NCBIN:46006, NCBI:46012)  
C:Keywords: fusion protein  
F:1-50/Region: retrovirus-like H3 promoter region derived  
F:51-102/Region: human calbindin-derived (fragment)

Query Match  
Best Local Similarity 72.2%; Score 39; DB 4; Length 102;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPT 9  
DB 25 LCNEDEPT 32

RESULT 3  
T40116  
hypothetical protein SPBC2D10.13 - fission yeast (Schizosaccharomyces pombe)  
C/Spectes: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
C/Accession: T40116  
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A/Reference number: Z21906  
A/Accession: T40116  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-490 <MOO>  
A/Cross-references: EMBL:AL031788; PIDN:CAA21171.1; GSPDB:GN00067; SPDB:SPBC2D10.13  
Experimental source: strain 972n-; cosmid c2D10  
Genetic:

QY 2 LCNEDEPT 8  
DB 237 LCSEDEPT 243

Query Match 72.2%; Score 39; DB 2; Length 490;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
UHH2  
interleukin-2 receptor alpha chain precursor [validated] - human  
N/Alternate names: CD25; Tac antigen  
N/Containing: Interleukin-2 receptor alpha chain, splice form 2  
C/Spectes: Homo sapiens (man)  
C/Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Dec-2000  
C/Accession: A44186; A24113; A01856; I57801; I52791; A61346; A33651; A34186; I52255  
R/Leonard, W.J.; Depper, J.M.; Kanehisa, M.; Koehnle, M.; Pelfer, N.J.; Svetlik, P.B.; S  
Science 220, 633-639, 1985  
A/Title: Structure of the human interleukin-2 receptor gene.  
A/Reference number: A44186; MUID:86018869; PMID:2996141  
A/Accession: A44186  
A/Molecule type: DNA  
A/Residues: 1-272 <LEO>  
A/Cross-references: GB:M10322  
R/Ishida, N.; Kanamori, H.; Noma, T.; Nishida, T.; Sabe, H.; Suzuki, N.; Shimizu, A.; H  
Nucleic Acids Res. 13, 7579-7589, 1985  
A/Title: Molecular cloning and structure of the human interleukin 2 receptor gene.  
A/Reference number: A24113; MUID:86061183; PMID:2999698  
A/Accession: A24113  
A/Molecule type: DNA  
A/Residues: 1-272 <ISH>  
A/Cross-references: GB:X03131; NID:G33818; PIDN:CAA26906.1; PID:G1200070  
R/Nikaido, T.; Shimizu, A.; Ishida, N.; Sabe, H.; Teshigawara, K.; Maeda, M.; Uchiyama,  
Nature 311, 631-635, 1984  
A/Title: Molecular cloning of cDNA encoding human interleukin-2 receptor.  
A/Reference number: A01856; MUID:85012734; PMID:6090949  
A/Accession: A01856  
A/Molecule type: mRNA  
A/Residues: 1-272 <NIK>  
A/Cross-references: GB:X01057; GB:X01058; GB:X01402; NID:G33812; PIDN:CAA25555.1; PID:G3  
R/Cosman, D.; Wignall, J.; Lewis, A.; Albert, A.; Cerretti, D.P.; Park, L.; Dower, S.K.;  
Mol. Immunol. 23, 935-941, 1986  
A/Title: High level stable expression of human interleukin-2 receptors in mouse cells ge  
A/Reference number: I57801; MUID:87064653; PMID:3097520  
A/Accession: I57801

A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 22-125, 'K', 127-262, 'Q', 264-272 <COS>  
A/Cross-references: GB:M1098; NID:G186307; PIDN:AAA59142.1; PID:G386820  
R/Cross, S.L.; Feinberg, M.B.; Wolf, J.B.; Holbrook, N.U.; Wong-Staal, F.; Leonard, W.J  
Cell 49, 47-56, 1987  
A/Title: Regulation of the human interleukin-2 receptor alpha chain promoter: activation  
A/Reference number: I52791; MUID:87159546; PMID:3030566  
A/Accession: I52791  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-21 <CRO>  
A/Cross-references: GB:M1864; NID:G186375; PIDN:AAA59162.1; PID:G553510  
R/Urdal, D.L.; March, C.J.; Gillis, S.; Larsen, A.; Dower, S.K.  
Proc Natl. Acad. Sci. U.S.A. 81, 6481-6485, 1984  
A/Title: Purification and chemical characterization of the receptor for interleukin 2 fr  
A/Reference number: A61346; MUID:85038539; PMID:6436815  
A/Accession: A61346  
A/Molecule type: protein  
A/Residues: 22-31 <URD>  
R/Miedel, M.C.; Hulmes, J.D.; Weber, D.V.; Bailon, P.; Pan, Y.C.E.  
Biochem. Biophys. Res. Commun. 154, 372-379, 1988  
A/Title: Structural analysis of recombinant soluble human interleukin-2 receptor. Primar  
A/Reference number: A33651; MUID:88280794; PMID:3134887  
A/Accession: A33651  
A/Molecule type: protein  
A/Residues: 22-244, 'P', <MIE1>  
A/Note: this soluble recombinant form binds IL-2  
R/Miedel, M.C.; Hulmes, J.D.; Pan, Y.C.E.  
J. Biol. Chem. 264, 21097-21105, 1989  
A/Title: Limited proteolysis of recombinant human soluble interleukin-2 receptor. Ident  
A/Reference number: A34186; MUID:90078206; PMID:2687272  
A/Accession: A34186  
A/Molecule type: protein  
A/Residues: 22-26; 56-62; 109-113; 119-123; 162-166 <MIE2>  
A/Note: use of recombinant protein and proteolysis allowed the authors to study the reg  
R/Mercken, L.; Moraes, V.; Hemon, L.; Lionne, B.; Bousseau, A.; Dautry-Varsat, A.; Collin  
Biochem. Biophys. Res. Commun. 180, 1390-1395, 1991  
A/Title: An exon 5-deleted mRNA encodes a functional interleukin 2 receptor alpha-subun  
A/Reference number: I52255; MUID:92062171; PMID:1840490  
A/Accession: I52255  
A/Status: translation not shown; translated from GB/EMBL/DBJ  
A/Residues: 193-194, 219-220 <MER>  
A/Molecule type: mRNA  
A/Residues: 193-194, 219-220 <MER>  
A/Cross-references: GB:S64248; NID:G238639; PIDN:AA820279.1; PID:G238640  
C/Comment: This receptor is sulfated, phosphorylated, and contains N- and O-linked carb  
C/Genetics:  
A/Gene: GDB:IL2RA  
A/Cross-references: GDB:119345; OMIM:147730  
A/Map position: 10p15-10p14  
A/Intons: 22/1; 86/1; 123/1; 195/1; 219/1; 243/1; 265/2  
C/Complex: The high affinity receptor is a heterotrimer of alpha, beta (see PIR:A30342),  
C/Function:  
A/Description: receptor for interleukin-2  
A/Pathway: Interleukin-2 stimulated growth and differentiation of T cells, B cells, NK  
C/Superfamily: Interleukin-2 receptor alpha chain; complement factor H repeat homology  
C/Keywords: alternative splicing; cytokine receptor; duplication; glycoprotein; heterotr  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:19-82/Domain: complement factor H repeat homology <FHI>  
F:22-272/Product: extracellular #status predicted <Ext>  
F:22-240/Domain: intracellular #status predicted <Int>  
F:22-194, 219-272/Product: interleukin-2 receptor alpha chain, splice form 2 #status pred  
F:22-88, 119-187/Region: interleukin-2 binding core  
F:125-184/Domain: complement factor H repeat homology <FHI>  
F:241-259/Domain: transmembrane #status predicted <TM>  
F:260-272/Domain: intracellular #status predicted <Int>  
F:24-168, 67-125, 152-184/Disulfide bonds: #status experimental  
F:49-80, 51-82/Disulfide bonds: (or 49-82, 51-80) #status experimental  
F:70, 89/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:218, 224, 229, 236, 237/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 70.4%; Score 38; DB 1; Length 272;  
Best Local Similarity 62.5%; Pred. No. 16;



Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDPP 8  
:|||||  
DB 22 ELCDDDPP 29

RESULT 5  
S62460  
hypothetical protein SPAC2G11.05c - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: T38571; S62460  
R:Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, October 1995  
A:Reference number: 221745  
A:Accession: T38571  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-701 <BA2>  
A:Cross-references: EMBL:254354; NID:G1019398; PIDN:CAA91170.1; PID:G1019403; GSPDB:GN00  
A:Experimental source: strain 972h-; cosmid c2G11  
C:Genetics:  
A:Gene: SPAC2G11.05c  
A:Map position: 1L

Query Match  
Best Local Similarity 68.5%; Score 37; DB 2; Length 701;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPP 8  
:|||||  
DB 122 LCNKKRP 128

RESULT 6  
T45738  
hypothetical protein F24M12.110 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T45738  
R:Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: 223012  
A:Accession: T45738  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-895 <VIT>  
A:Cross-references: EMBL:AL132980  
A:Experimental source: cultivar Columbia; BAC clone F24M12  
C:Genetics:  
A:Map position: 3  
A:Introns: 435/3; 485/3; 613/1; 671/2; 762/2; 827/2  
A>Note: F24M12.110

Query Match  
Best Local Similarity 68.5%; Score 37; DB 2; Length 895;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CNEDPPT 9  
:|||||  
DB 408 CPEDPPT 414

RESULT 7  
A38234  
oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - human  
N:Alternate names: 2-oxoglutarate:lipoamide 2-oxidoeductase; alpha-ketoglutarate dehydr  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Oct-1999  
C:Accession: A38234  
R:Kolke, K.; Urata, Y.; Goto, S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 1963-1967, 1992

A>Title: Cloning and nucleotide sequence of the cDNA encoding human 2-oxoglutarate dehyd  
A:Reference number: A38234; MUID:92179301; PMID:1542694  
A:Accession: A38234  
A:Molecule type: mRNA  
A:Residues: 1-1003 <KO1>  
A:Cross-references: GB:D10523  
A:Experimental source: fetal liver  
A>Note: sequence extracted from NCBI backbone (NCBI:87352)  
C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom  
C:Keywords: mitochondrion; oxidoreductase; thiamin pyrophosphate; tricarboxylic acid cyc  
F:1-4/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F:41-1003/Product: oxoglutarate dehydrogenase (lipoamide) #status predicted <MAT>  
F:408-453/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match  
Best Local Similarity 68.5%; Score 37; DB 2; Length 1003;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDP 7  
:|||||  
DB 801 QWCNDPP 807

RESULT 8  
T49683  
probable oxoglutarate dehydrogenase precursor [imported] - Neurospora crassa  
N:Alternate names: protein B8B20.370  
C:Species: Neurospora crassa  
C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jun-2000  
C:Accession: T49683  
R:Schulte, U.; Algn, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: 225022  
A:Accession: T49683  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1022 <SCH>  
A:Cross-references: EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.370  
A:Experimental source: BAC clone B8B20; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B8B20.370  
A:Map position: 6  
A:Introns: 27/3; 843/1  
C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom

Query Match  
Best Local Similarity 68.5%; Score 37; DB 2; Length 1022;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNEDP 7  
:|||||  
DB 794 LCNEDP 799

RESULT 9  
T26868  
hypothetical protein Y43F8C.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26868  
R:Ainscough, R.  
submitted to the EMBL Data Library, October 1998  
A:Reference number: 220279  
A:Accession: T26868  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-245 <WIL>  
A:Cross-references: EMBL:AL032637; PIDN:CAA21609.1; CESP:Y43F8C.5  
A:Experimental source: clone Y43F8C  
C:Genetics:  
A:Gene: CESP:Y43F8C.5  
A:Introns: 69/3; 163/2

Query Match 66.7%; Score 36; DB 2; Length 245;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
Db 192 LCNEDPPT 199

## RESULT 10

T16350  
hypothetical protein F42G9.8 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jan-2000

C:Accession: T16350

R:Taich, A.

Submitted to the EMBL Data Library, March 1996

A:Description: The sequence of *C. elegans* cosmid F42G9.

A:Reference number: Z18498

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T16350

A:Residues: 1-359 <TAI>

A:Cross-references: EMBL:U00051; NID:g1216305; PID:g1216308; PIDN:AAA91354.1; CESP:F42G9

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F42G9.8

A:Insertions: 28/2; 50/2; 113/2; 155/3; 220/3; 290/2

C:Superfamily: *Caenorhabditis elegans* hypothetical protein F42G9.8

Query Match 66.7%; Score 36; DB 2; Length 359;  
Best Local Similarity 66.7%; Pred. No. 50;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QCNEDPPT 9  
Db 166 RLCNKDPPT 174

## RESULT 11

T10677

pathogenesis-related protein homolog F3L17.40 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T10677

R:Bayan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.

Submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16652

A:Accession: T10677

A:Residues: 1-185 <BEV>

A:Cross-references: EMBL:AL080283; GSPDB:GN00062; ATSP:F3L17.40

A:Experimental source: cultivar Columbia; BAC clone F3L17

C:Genetics:

A:Gene: ATSP:F3L17.40

A:Map position: 4

C:Superfamily: pathogenesis-related leaf protein

Query Match 64.8%; Score 35; DB 2; Length 185;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 8  
Db 170 ICNNDPPT 176

## RESULT 12

C75518  
streptomycin 3-kinase - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: C75518

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zaleski, C.; M.  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: C75518

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-283 <WHI>

A:Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAF10031.1; PID:g645813

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0455

A:Map position: 1

C:Superfamily: streptomycin 6-kinase

Query Match 64.8%; Score 35; DB 2; Length 283;  
Best Local Similarity 75.0%; Pred. No. 60;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9  
Db 213 LCNEDPPT 220

## RESULT 13

T11633

hypothetical protein - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 20-Jun-2000

C:Accession: T11633

R:Barrell, B.G.; Rajandream, M.A.; Wood, V.

Submitted to the EMBL Data Library, September 1997

A:Reference number: Z17303

A:Accession: T11633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <BAR>

A:Cross-references: EMBL:Z99260

C:Genetics:

A:Map position: 1L

A:Note: SPAC3A11.11c

C:Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 64.8%; Score 35; DB 2; Length 334;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CNEQPPS 235  
Db 229 CNEQPPS 235

## RESULT 14

T42755

tyrosyl-protein sulfoxidase homolog - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T42755

R:Moore, K.L.; Ouyang, Y.B.

J. Biol. Chem. 273, 24770-24774, 1998

A:Title: Molecular cloning and expression of human and mouse tyrosyl-protein sulfoxidase

A:Reference number: Z22262; MUID:98406128; PMID:9733778

A:Accession: T42755

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-380 <MOO>

A:Cross-references: EMBL:AF049709; NID:g3617847; PIDN:AA036062.1; PID:g3617848

Query Match 64.8%; Score 35; DB 2; Length 380;  
Best Local Similarity 66.7%; Pred. No. 81;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QUCNEDPT 9  
 DB 155 RLCNKDPFT 163

RESULT 15

JE0276  
 Voltage-gated potassium channel alpha chain Kv9.3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 08-Dec-2000  
 C:Accession: JE0276  
 R:Stocker, M.; Kerchenshteiner, D.  
 Biochem. Biophys. Res. Commun. 248, 927-934, 1998  
 A:Title: Cloning and tissue distribution of two new potassium channel alpha-subunits from  
 A:Reference number: JE0275; WUID:98369652; PMID:9704029  
 A:Accession: JE0276  
 A:Molecule type: mRNA  
 A:Residues: 1-491 <STO>  
 Cross-references: GB:Y17607  
 Description: potassium channel protein dkl1

Query Match 64.8%; Score 35; DB 2; Length 491;  
 Best Local Similarity 83.3%; Pred. No. 1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 CNEDEPT 8  
 DB 424 CSEDEPT 429

Search completed: September 10, 2003, 17:42:44  
 Job time : 14.15 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:37:57 : Search time 30.8 Seconds  
(without alignments)  
92.162 Million cell updates/sec

Title: US-09-759-112A-19  
Perfect score: 55  
Sequence: 1 RVSLEYAMDY 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRINUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39	70.9	167	5	002369	002369 chironomus
2	38	69.1	164	16	082N46	082N46 salmonella
3	38	69.1	164	16	082N47	082N47 salmonella
4	37	67.3	183	4	09H616	09H616 homo sapien
5	37	67.3	190	4	09NT91	09NT91 homo sapien
6	37	67.3	322	17	09TC16	09TC16 thermoplasma
7	37	67.3	387	16	08DVU3	08DVU3 streptococcus
8	37	67.3	391	4	09NXV7	09NXV7 homo sapien
9	37	67.3	1712	4	081Y21	081Y21 homo sapien
10	36	65.5	255	16	08DCL2	08DCL2 vibrio vuln
11	36	65.5	275	17	0972D4	0972D4 sulfobolus
12	36	65.5	286	12	0908H7	0908H7 myxoma viru
13	36	65.5	359	16	08FKD3	08FKD3 xanthomonas
14	36	65.5	454	16	095WT9	095WT9 streptomyc
15	35	63.6	145	5	09GUY2	09GUY2 polyanthroc
16	35	63.6	210	16	08DRS5	08DRS5 streptococc

17	35	63.6	345	16	09X7P7	09X7P7 streptomyc
18	35	63.6	332	12	091BD6	091BD6 spodoptera
19	35	63.6	463	2	09RN63	09RN63 streptomyc
20	35	63.6	556	5	081PL3	081PL3 drosophila
21	35	63.6	1216	10	08W1P1	08W1P1 oryza sativ
22	34	61.8	192	2	050403	050403 methyllobact
23	34	61.8	314	16	092TR9	092TR9 rhizobium m
24	34	61.8	391	11	091V12	091V12 mus musculu
25	34	61.8	742	2	08KZS8	08KZS8 acetobacter
26	34	61.8	742	2	053362	053362 acetobacter
27	34	61.8	767	17	09H1D7	09H1D7 thermoplasma
28	34	61.8	812	16	08REC9	08REC9 fusobacteri
29	34	61.8	880	10	09FID9	09FID9 arabidopsis
30	34	61.8	880	10	08RW00	08RW00 arabidopsis
31	34	61.8	887	2	09RGU0	09RGU0 salmonella
32	34	61.8	893	2	09LSU7	09LSU7 salmonella
33	34	61.8	893	16	0935F3	0935F3 salmonella
34	34	61.8	1653	16	08XAY3	08XAY3 escherichia
35	34	61.8	1653	16	08CVT2	08CVT2 escherichia
36	33	60.0	99	2	09F8J2	09F8J2 carboxydoch
37	33	60.0	134	4	096GJ9	096GJ9 homo sapien
38	33	60.0	148	10	09LER7	09LER7 arabidopsis
39	33	60.0	148	10	09AB31	09AB31 arabidopsis
40	33	60.0	153	17	08TK61	08TK61 methanosa
41	33	60.0	167	5	015588	015588 entamoeba h
42	33	60.0	174	16	098GL3	098GL3 rhizobium l
43	33	60.0	178	2	09APR9	09APR9 carboxydoch
44	33	60.0	249	16	08H864	08H864 agrobacteri
45	33	60.0	293	16	086594	086594 streptomyc

## ALIGNMENTS

## RESULT 1

ID 002369 PRELIMINARY; PRT; 167 AA.

AC 002369; 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

GN Globin XII.

OS Chironomus thummi thummi (Midge).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;

OC Chironomidae; Chironominae; Chironomus.

OX NCBI\_TaxID=7155;

RP SEQUENCE FROM N.A.

RX MEDLINE=94275867; PubMed=8006991;

RA Kao W.Y., Trewitt P.M., Bergtrom G.;

RT "Intron-containing globin genes in the insect Chironomus thummi.";

RL J. Mol. Evol. 38:241-249(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Gruhl M.C., Kao W.-Y., Bergtrom G.;

RT "Evolution of Orthologous Intronless and Intron-Bearing Globin Genes in Two Insect Species.";

RL J. Mol. Evol. 0:0-0(1997).

DR EMBL; AF001292; AAB58934.1; -

DR HSSP; P02229; IECA.

DR InterPro; IPR002336; Erythrcurin.

DR InterPro; IPR000971; Globin.

DR Pfam; PF00042; globin; 1.

DR PRINTS; PR00611; ERYTHRCURIN.

DR PROSITE; PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport

SO SEQUENCE 167 AA; 18428 MW; 551F5ASDFC3E7742 CRC64;

Query Match 70.9%; Score 39; DB 5; Length 167;

Best Local Similarity 72.7%; Pred. No. 5.5;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAYAMDY 11  
DB 126 RVSLTAYLADH 136

## RESULT 2

Q8ZNA6 PRELIMINARY; PRT; 1644 AA.  
AC Q8ZNA6;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Putative inner membrane lipoprotein.  
GN STM2532.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602;  
[1]

SEQUENCE FROM N.A.  
STRAIN=L72 / SCS1412 / ATCC 700720;  
MEDLINE=2153494; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewel N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
RT L72."  
RL Nature 413:852-856(2001).  
DR EMBL; AB008815; AL21426.1; -;  
KM Lipoprotein; Hypothetical protein; Complete proteome.  
SQ SEQUENCE 1644 AA; 179646 MW; BCF7A526BD629CA1 CRC64;

Query Match 69.1%; Score 38; DB 16; Length 1644;  
Best Local Similarity 87.5%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTVAYAMDY 11  
DB 1245 LTVAYAMDY 1252

RESULT 3  
Q8ZAN7 PRELIMINARY; PRT; 1644 AA.  
Q8ZAN7;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Putative lipoprotein.  
GN STY2778.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=601;  
[1]

SEQUENCE FROM N.A.  
STRAIN=CT18;  
AC STRAIN=CT18;  
MDLINE=2153494; PubMed=11677608;  
RA Churchill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C., Dougan K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Baker S., Basham D., Brooks R., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.W., Dowd L., White N., Farrar J.,  
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jørgensen K.,  
RA Krogh A., Larsen T.S., Leather S., Mølle S., O'Garra P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrett B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar Typhimurium CT18."  
RL Nature 413:848-852(2001).  
DR EMBL; AL627275; CAD02735.1; -;

KW Lipoprotein; Hypothetical protein; Complete proteome.  
SQ SEQUENCE 1644 AA; 179378 MW; D8341677631A70DF CRC64;

Query Match 69.1%; Score 38; DB 16; Length 1644;  
Best Local Similarity 87.5%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTVAYAMDY 11  
DB 1245 LTVAYAMDY 1252

## RESULT 4

Q9H616 PRELIMINARY; PRT; 183 AA.  
AC Q9H616;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein FLJ22680.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]

SEQUENCE FROM N.A.  
STRAIN=Small intestine;  
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,  
RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,  
RA Nakamura Y., Isono T., Sugano S.;  
RT "NEDD human cDNA sequencing project."  
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK026333; BA15451.1; -;  
DR EMBL; BC020601; AA120601.1; -;  
KM Hypothetical protein.  
SQ SEQUENCE 183 AA; 20827 MW; 6E33085B02A41194 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 183;  
Best Local Similarity 54.5%; Pred. No. 16;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLTAYAMDY 11  
DB 106 RVSLTAYALDF 116

## RESULT 5

Q9NT91 PRELIMINARY; PRT; 190 AA.  
AC Q9NT91;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN DKFZP434E1722.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]

SEQUENCE FROM N.A.  
STRAIN=Testis;  
AC BLUM H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;  
RA BLUM H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;  
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL137464; CAB70751.1; -;  
KM Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 190 AA; 21833 MW; D9C9D7BCDE006CE9 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 190;  
 Best Local Similarity 54.5%; Pred. No. 16;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSITAYAMDY 11  
 ::|||::|  
 Db 127 KMSLNAYALDF 137

## RESULT 6

097CJ6 PRELIMINARY; PRT; 322 AA.  
 AC 097CJ6;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein TV0105.  
 TV0105 OR TVG0110910.  
 Thermoplasma volcanium.  
 Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
 OC Thermoplasmataceae; Thermoplasma.  
 OX NCBI\_TaxID=50339;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GS1 / DSM 4239 / JCM 9571;  
 RX MEDLINE=20570466; PubMed=11121031;  
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,  
 Kawashima O-hya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,  
 RA Nunoshita T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,  
 RT "Archaeal adaptation to higher temperatures revealed by genomic  
 sequence of Thermoplasma volcanium."  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).  
 DR EMBL; AP000991; BAB59247.1;  
 DR InterPro; IPR002729; DUF48.  
 DR Pfam; PF01867; DUF48; 1.  
 DR ProDom; PD008695; DUF48; 1.  
 DR TIGRFAMs; TIGR00287; TIGR00287; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 322 AA; 37255 MW; 5FB6133DABE746C8 CRC64;

Query Match 67.3%; Score 37; DB 17; Length 322;  
 Best Local Similarity 54.5%; Pred. No. 28;  
 Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVSITAYAMDY 11  
 ::|||::|  
 Db 43 KVSLSWALDY 53

## RESULT 7

08DVU3 PRELIMINARY; PRT; 387 AA.  
 AC 08DVU3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 SMU.372.  
 GN Streptococcus mutans.  
 OS Streptococcus mutans.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1309;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
 RX MEDLINE=22295063; PubMed=12397186;  
 RA Ajdic D., McShan W.M., McLaughlin R.B., Savic G., Chang J.,  
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,  
 Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferreretti J.J.,  
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 pathogen."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

DR EMBL; AE014885; AAN58130.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 387 AA; 45217 MW; 46F6D2F75FE69CE0 CRC64;

Query Match 67.3%; Score 37; DB 16; Length 387;  
 Best Local Similarity 63.6%; Pred. No. 35;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RVSITAYAMDY 11  
 ::|||::|  
 Db 220 RSLTNYTADY 230

## RESULT 8

09NXV7 PRELIMINARY; PRT; 391 AA.  
 AC 09NXV7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein FLJ20035.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Colon;  
 RA Kawabata A., Hixji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Oca T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,  
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK000042; BA90901.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 391 AA; 44697 MW; BF9A267A7ED1BA6B CRC64;

Query Match 67.3%; Score 37; DB 4; Length 391;  
 Best Local Similarity 54.5%; Pred. No. 35;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSITAYAMDY 11  
 ::|||::|  
 Db 314 KMSLNAYALDF 324

## RESULT 9

081Y21 PRELIMINARY; PRT; 1712 AA.  
 AC 081Y21;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ20035.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Brain;  
 RA Strausberg R.,  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC038115; AAH38115.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 1712 AA; 197824 MW; ES1D3588135D2066 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 1712;  
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSITAYAMDY 11  
 ::|||::|

Db 1635 KMSLNAYALDF 1645

## RESULT 10

08DCL2 PRELIMINARY; PRT; 255 AA.  
AC 08DCL2;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Putative salt-induced outer membrane protein.  
GN VVI1391.  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxId=672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
Chey H.E.;  
"Complete genome sequence of Vibrio vulnificus CMCP6,"  
Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF016801; AAC09840.1; -  
KM Complete proteome.  
SQ SEQUENCE 255 AA; 28971 MW; 8ACAB07128790F68 CRC64;

Query Match 65.5%; Score 36; DB 16; Length 255;  
Best Local Similarity 88.9%; Pred. No. 36;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 VSLTAYAMD 10  
16 VSLTAYAD 24

## RESULT 11

0972D4 PRELIMINARY; PRT; 275 AA.  
AC 0972D4;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Hypothetical protein S1194.  
GN S1194.  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Thermoprocei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
NCBI\_TaxId=11955;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=JCM 10545 / 7;  
RA PubMed=11572479;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
Sakine M., Baba S.-I., Anai A., Kouguchi H., Hosoyama A., Fukui S.,  
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,  
Aoki K.-I., Maeda S., Yanagii M., Nishimura M., Yamagishi A.,  
Oshima T., Kikuchi H.;  
"Complete genome sequence of an aerobic thermophilic  
RT Crenarchaeon, Sulfolobus tokodaii strain7,"  
RL DNA Res. 8:123-140(2001).  
DR EMBL; AP000985; BAB66235.1; -  
DR InterPro; IPR006638; E1p3.1;  
DR SMART; SM00729; E1p3.1;  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 275 AA; 32042 MW; 869625BD4FC3027 CRC64;

Query Match 65.5%; Score 36; DB 17; Length 275;  
Best Local Similarity 63.6%; Pred. No. 39;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 RVSILTAYAMDY 11

Db 22 KVSETAYALOY 32

## RESULT 12

0908H7 PRELIMINARY; PRT; 286 AA.  
AC 0908H7;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE M124R.  
GN M124R.  
OS Myxoma virus (strain Lausanne).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Leporipoxvirus.  
OX NCBI\_TaxId=31530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Lausanne;  
RX MEDLINE=20032073; PubMed=10562494;  
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,  
Macalvey C., Miller D., Evans D., McFadden G.;  
"The complete DNA sequence of myxoma virus,"  
RT Virology 264:298-318(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Lausanne;  
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.-X.,  
Macalvey C., Miller D., Evans D., McFadden G.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF170726; AAF15012.1; -  
SQ SEQUENCE 286 AA; 32627 MW; 90C638BAE0AF7546 CRC64;

Query Match 65.5%; Score 36; DB 12; Length 286;  
Best Local Similarity 54.5%; Pred. No. 40;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 RVSILTAYAMDY 11  
4 RVSIVSHVDY 14

## RESULT 13

08PKD3 PRELIMINARY; PRT; 369 AA.  
AC 08PKD3;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Plasmid-related protein.  
GN ORF10 OR XAC2242.  
OS Xanthomonas axonopodis (pv. citri).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.  
NCBI\_TaxId=92829;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=306 / ATCC 13902 / XY 101;  
RX MEDLINE=2202145; PubMed=12024217;  
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
Camarote G., Camarvan F., Cardozo J., Chamberg F., Chiapina L.P.,  
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,  
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
RA Spínola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,



RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities.";  
 RL Nature 417:459-463(2002).  
 DR EMBL: AE011861; AAM37095.1; -;  
 DR InterPro: IPR002226; N12N6\_mtfase.  
 DR InterPro: IPR002052; N6\_Mcase.  
 DR InterPro: IPR000051; SAM\_bind.  
 DR PRINTS: PR00507; N12N6MTRFAS.  
 DR PROSITE: PS00092; N6\_MTASE; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 369 AA; 40745 MW; 754FD19FA44F84E0 CRC64;  
 Query Match 65.5%; Score 36; DB 16; Length 369;  
 Best Local Similarity 54.5%; Pred. No. 53;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RVSLTYAMDY 11  
 DB 61 RAOVTAVAVY 71  
 RESULT 14  
 Q9EW79 PRELIMINARY; PRT; 454 AA.  
 ID Q9EW79;  
 AC Q9EW79;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative secreted protease.  
 GN SC00732 OR 3SC5B7.10.  
 OS Streptomyces coelicolor.  
 OC Streptomyces coelicolor; Actinobacteria; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomyces.  
 NCBI\_TaxID=1902;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Seeger K.J., Harris D.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Parthill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL939106; CAC14934.1; -;  
 DR HSP; Pali40; ZSFA.

DR InterPro: IPR004236; AL\_protease.  
 DR InterPro: IPR001316; Endoprotease2A.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF02983; AL\_protease; 1.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00861; ALTYICPTASE.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS00134; TRYP\_SIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYP\_SIN\_SER; 1.  
 KW Hydrolase; Protease; Serine protease; Complete proteome.  
 SQ SEQUENCE 454 AA; 46273 MW; 8708E7726D0DD1D9 CRC64;  
 Query Match 65.5%; Score 36; DB 16; Length 454;  
 Best Local Similarity 63.6%; Pred. No. 66;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RVSLTYAMDY 11  
 DB 119 RVAGTAMALDY 129  
 RESULT 15  
 Q9GUY2 PRELIMINARY; PRT; 145 AA.  
 ID Q9GUY2;  
 AC Q9GUY2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE C-type lectin TC14-1.  
 GN TC14-1.  
 OS Polyandrocampa misakiensis.  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Styelidae; Polyandrocampa.  
 NCBI\_TaxID=7723;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Matsumoto J., Fujiwara S., Yubisui T., Kawamura K.;  
 RT "Cytostatic activity of C-type lectins on multipotent epithelial cells  
 RT in budding tunicates.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB049563; BAB16304.1; -;  
 DR InterPro: IPR001304; Lectin\_C.  
 DR Pfam: PF00059; lectin\_cg; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Lectin.  
 SQ SEQUENCE 145 AA; 16056 MW; 87DAC389C9DCD59D CRC64;  
 Query Match 63.6%; Score 35; DB 5; Length 145;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 TAYAMDY 11  
 DB 17 TSYAMDY 23

Search completed: September 10, 2003, 17:42:03  
 Job time : 33.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:34:47; Search time 11 Seconds

(without alignments)  
47.027 Million cell updates/sec

Title: US-09-759-112a-19

Perfect score: 55  
Sequence: 1 RVS1TAYAMDY 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.8	370	1	PNK3_HUMAN	Q9h999 homo sapien
2	61.8	370	1	PNK3_MOUSE	Q8r2w9 mus musculu
3	61.8	388	1	ALR_BACHD	Q9kff9 bacillus ha
4	61.8	599	1	YJUI_YEAST	32525 saccharomyc
5	61.8	738	1	DHERT_ACEPO	P28033 acetoabacter
6	61.8	739	1	DHERT_ACEBU	Q44002 acetoabacter
7	61.8	742	1	DHERT_ACEAC	P18278 acetoabacter
8	61.8	757	1	DHERT_GLUOX	O05542 gluconobact
9	61.8	803	1	DCML_HYDPS	P19913 hydrogenuph
10	61.8	1653	1	YFHM_ECOLI	P76578 escherichia
11	60.0	302	1	YAJF_ECOLI	P23917 escherichia
12	60.0	548	1	PNK1_MOUSE	Q8k4k6 mus musculu
13	60.0	570	1	PNK2_HUMAN	Q9b423 homo sapien
14	60.0	598	1	PNK1_HUMAN	Q8t604 homo sapien
15	60.0	1115	1	DP3A_BACSU	O34623 bacillus su
16	58.2	127	1	GC62_PSEAE	Q91136 pseudomonas
17	58.2	150	1	VIL1_HYV67	P50825 human papil
18	58.2	182	1	APT_PSEAE	Q04633 pseudomonas
19	58.2	329	1	MRAV_LACLA	Q9c7f0 lactococcus
20	58.2	360	1	RFT_PASMU	P57552 pasteurella
21	58.2	490	1	IFT4_HUMAN	O14579 homo sapien
22	58.2	985	1	INVA_YERPS	P11922 yerinia ps
23	58.2	1230	1	UG64_SOLTU	Q43846 solanum tub
24	56.4	97	1	CMGC_BACLI	Q8v471 bacillus li
25	56.4	134	1	YBIM_ECOLI	P75781 escherichia
26	56.4	185	1	ADH_ANNPL	P30350 anaer piaty
27	56.4	189	1	PAAD_NEIMA	Q9jw78 neisseria m
28	56.4	189	1	PAAD_NEIMA	Q9jw78 neisseria m
29	56.4	268	1	YC73_HAEIN	P44550 haemophilus
30	56.4	268	1	YC73_HAEIN	P44550 haemophilus
31	56.4	311	1	PPAC_STRPY	Q94192 streptococc
32	56.4	340	1	OMP2_CHLTR	P38006 chlamydia t
33	56.4	355	1	RFL_CAMJE	Q9p663 campylobact

34	31	56.4	359	1	RPI_BRUME	Q8y195 bruceella me
35	31	56.4	359	1	RPI_RHILLO	Q98993 rhizobium 1
36	31	56.4	360	1	RPI_AGRTS	Q8ab88 agrobacteri
37	31	56.4	360	1	RPI_ECOLI	P07011 escherichia
38	31	56.4	360	1	RPI_RHIME	Q92mk5 rhizobium m
39	31	56.4	360	1	RPI_SALTY	P13654 salmoneila
40	31	56.4	360	1	RPI_YERPE	Q8z6x8 yerinia pe
41	31	56.4	361	1	RPI_COXBU	P47849 coxiella bu
42	31	56.4	361	1	RPI_HAEIN	P43917 haemophilus
43	31	56.4	441	1	DHWT_TAXCA	O81169 taxus canad
44	31	56.4	453	1	SYS_ARCFU	O28244 archaeeoglob
45	31	56.4	464	1	GRA3_RAT	P24524 rattus norv

## ALIGNMENTS

RESULT 1  
ID PNK3\_HUMAN STANDARD; PRT; 370 AA.  
AC Q9h999;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Pantothenate kinase 3 (EC 2.7.1.33) (Pantothenic acid kinase 3)  
DE (hpank3).  
GN PANK3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Itoigai T., Ota T., Hayashi K., Sugiyama T., Otaki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takenuchi K.,  
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuko Y., Oshima A.,  
RT "NEO human cDNA sequencing project";  
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Altschul S.F., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stalderon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,  
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=21372465; PubMed=11479594;  
RA Zhou B., Westway S.K., Levinson B., Johnson M.A., Gitschler J.,  
RA Haylick S.J.;  
RT "A novel pantothenate kinase gene (PANK2) is defective in  
Hallerorden-Spatz syndrome";  
RL Nat. Genet. 28:345-349(2001).  
CC -!- FUNCTION: Plays a role in the physiological regulation of the

```
CC intracellular CoA concentration (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
CC thioesters (By similarity).
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Highly expressed in the liver.
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AK022961; BAB1433.1; -.
CC EMBL; BC013705; AAH13705.1; -.
CC Genew; HGNC; 19365; PANK3.
CC MIM; 606161; -.
CC InterPro; IPR004567; Pank_eukar.
CC DR Pfam; PF03630; Fumble; 1.
CC KM Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis.
CC SO SEQUENCE 370 AA; 41094 MW; 71EPA56079F352D CRC64;

Query Match 61.8%; Score 34; DB 1; Length 370;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 2 VSLTAYAMDY 11
Db 331 MKLALVALDY 340

RESULT 2
PANK3_MOUSE
ID PANK3_MOUSE STANDARD; PRT; 370 AA.
AC QGR2M9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pantothenate kinase 3 (EC 2.7.1.33) (Pantothenic acid kinase 3)
DE (PANK3).
GN PANK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Plange S.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kizyivski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.W., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Plays a role in the physiological regulation of the
CC intracellular CoA concentration (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
CC thioesters (By similarity).
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; BC027089; AAH27089.1; -.
CC DR EMBL; BC032188; AAH32188.1; -.
CC MGD; MGI:2387464; Pank3.
CC DR InterPro; IPR004567; Pank_eukar.
CC DR Pfam; PF03630; Fumble; 1.
CC KM Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis.
CC SO SEQUENCE 370 AA; 41120 MW; 61D982A619E83A78 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 370;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 2 VSLTAYAMDY 11
Db 331 MKLALVALDY 340

RESULT 3
ALR_BACHD
ID ALR_BACHD STANDARD; PRT; 388 AA.
AC QGKFP9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
DE ALR OR BH0520.
GN ALR OR BH0520.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=86665;
[1]
RP SEQUENCE FROM N.A.
RP STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -1- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -1- SIMILARITY: Belongs to the alanine racemase family.
CC -----
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CC -----
DR EMBL: AP001508; BAB04239.1; -.
DR PIR: H83714; H83714.
DR HSSP: P10724; 1BD0.
DR HAMAP: MF_01201; -. 1.
DR InterPro: IPR000821; Ala_racemase.
DR Pfam: PF00842; Ala_racemase_C; 1.
DR Pfam: PF01168; Ala_racemase_N; 1.
DR PRINTS: PRO0992; ALARACEMASE.
DR TIGRfam: TIGR00492; alr; 1.
DR PROSITE: PS00395; ALANINE_RACEMASE; 1.
DR Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KM Complete proteome.
FT ACT_SITE 40 40 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
FT ACT_SITE 40 40 SIMILARITY).
FT ACT_SITE 269 269 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
FT ACT_SITE 269 269 SIMILARITY).
FT BINDING 40 40 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 388 AA; 44020 MW; 8017C15D03C9A66A CRC64;
Query Match 61.8%; Score 34; DB 1; Length 388;
Best Local Similarity 45.5%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RVSUTAYAMDY 11
Db 101 RITLFYVQLDW 111

RESULT 4
ID YU1 YEAST STANDARD; PRT; 599 AA.
AC P32525;
DT 01-OCT-1993 (rel. 27, Created)
DT 01-FEB-1995 (rel. 31, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Hypothetical 68.5 kDa protein in PRP21-UBP12 intergenic region.
GN YUL201W OR J0325.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes;
OC NCBI_TaxId=4932;
OK [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95274326; PubMed=7754713;
Purnelle B., Coster P., Goffeau A.;
"The sequence of a 36 kb segment on the left arm of yeast chromosome
X identifies 24 open reading frames including NUC1, PRP21 (SP91),
CDC6, CRV2, the gene for S24, a homologue to the acetylase gene ACO1
and two homologues to chromosome III genes."
RT Yeast 10:1235-1249(1994).
RL [2]
RN SEQUENCE OF 1-323 FROM N.A.
RA MEDLINE=93342071; PubMed=8341697;
Arenas J.E., Abelson J.N.;
"The Saccharomyces cerevisiae PRP21 gene product is an integral
component of the preplisosome."
RT Proc. Natl. Acad. Sci. U.S.A. 90:6771-6775(1993).
RL [1]
CC -1- SIMILARITY: Contains 1 Rho-GAP domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X77688; CAA54756.1; -.
DR EMBL: Z49476; CAA89496.1; -.
DR EMBL: L07744; AAB09602.1; -.
DR PIR: S46630; S46630.

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DR SGD: S0003737; ECM25.
DR GO: GO:0007047; P:cell wall organization and biogenesis; IMP.
DR InterPro: IPR000198; RhogAP.
DR SMART: SM00324; RhogAP; 1.
DR PROSITE: PS50238; RHOGAP; 1.
DR Hypothetical protein.
KW DOMAIN 181 359
SQ SEQUENCE 599 AA; 68463 MW; 0A23F564E04597DE CRC64;
Query Match 61.8%; Score 34; DB 1; Length 599;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RVSUTAYAMDY 11
Db 157 RITLVVLYDY 167

RESULT 5
ID DHET ACEPO STANDARD; PRT; 738 AA.
AC P28036;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).
GN ADHA.
OS Acetobacter polyxogenes.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OK NCBI_TaxId=439;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91159482; PubMed=2001402;
Tawamki T., Fukaya M., Takemura H., Tayama K., Okumura H.,
Kawakura Y., Nishiyama M., Horiouchi S., Beppu T.;
"Cloning and sequencing of the gene cluster encoding two subunits of
membrane-bound alcohol dehydrogenase from Acetobacter polyxogenes."
RT Biochim. Biophys. Acta 1088:297-300(1991).
RL Biochim. Biophys. Acta 1088:297-300(1991).
CC -1- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPT: METHANOL).
CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde +
CC reduced acceptor.
CC -1- COFACTOR: POO AND HEME.
CC -1- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO
CC SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGENASE
CC COMPLEX.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
CC SPACE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
CC -1- SIMILARITY: Contains 1 cytochrome c domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D00635; BAA00528.1; -.
DR PIR: S14270; S14270.
DR HSSP: 09Z4J7; 1PLG.
DR InterPro: IPR001479; Bac_POO.
DR InterPro: IPR002372; Bac_POO_repeat.
DR Pfam: PF01011; Bacterial_POO; 3.
DR SMART: SM00564; POO; 3.
DR PROSITE: PS00363; BACTERIAL_POO_1; 1.
DR PROSITE: PS00364; BACTERIAL_POO_2; 1.
DR PROSITE: PS00190; CYTOCHROME_C_1; 1.
DR Oxidoreductase; POO; Heme; Membrane; Signal.
FT SIGNAL 1 35
FT SIGNAL 35

```

Query Match  
Best Local Similarity 70.0%; Pred. No. 39;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

61.8%; Score 34; DB 1; Length 738;

1 RVSLTYAMD 10  
|:|||||  
|:|||||

Db 685 RGALTAYGMD 694

RESULT 6  
DHET\_ACEU STANDARD; PRT; 739 AA.

Q44002; 007952;  
15-DEC-1998 (Rel. 37, Last sequence update)  
15-DEC-1998 (Rel. 37, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).  
ADH.  
Acetobacter europaeus.  
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Acetobacteraceae; Gluconacetobacter.  
NCBI\_TaxID=33995;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-DES11 / DSM 6160;  
RA Thurner C.A.K.;  
Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

-1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde + reduced acceptor.  
-1- COFACTOR: POQ AND HEME (BY SIMILARITY).  
-1- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX (BY SIMILARITY).  
-1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC SPACE (POTENTIAL).  
-1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.  
-1- SIMILARITY: Contains 1 cytochrome c domain.

-----  
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-----

CC EMBL; X82894; CAAS8066.1; -  
CC EMBL; Y09480; CAY70688.1; -  
CC HSSP; Q924J7; 1FLG.  
CC InterPro; IPR001479; Bac\_POQ.  
CC InterPro; IPR002372; Bac\_POQ\_repeat.  
CC InterPro; IPR000345; CytC\_heme\_bind.  
CC Pfam; PF01011; Bacterial\_POQ\_3.  
CC SMART; SM00564; POQ\_3.  
CC PROSITE; PS00363; BACTERIAL\_POQ\_1; 1.  
CC PROSITE; PS00364; BACTERIAL\_POQ\_2; 1.  
CC PROSITE; PS00190; CYTOCHROME\_C\_1.  
CC Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.  
CC SIGNAL 1 35  
CC CHAIN 36 739 ALCOHOL DEHYDROGENASE [ACCEPTOR].  
CC DOMAIN 635 739 CYTOCHROME C-LIKE.  
CC BINDING 651 651 HEME (COVALENT) (BY SIMILARITY).  
CC BINDING 654 654 HEME (COVALENT) (BY SIMILARITY).  
CC METAL 655 655 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 739 AA; 80944 MW; E681BB237ACB91F4 CRC64;

Query Match  
Best Local Similarity 70.0%; Pred. No. 39;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

61.8%; Score 34; DB 1; Length 739;

1 RVSLTYAMD 10  
|:|||||  
|:|||||

Db 686 RGALTAYGMD 695

RESULT 7  
DHET\_ACEAC STANDARD; PRT; 742 AA.

Q44002; 007952;  
01-NOV-1990 (Rel. 16, Created)  
01-NOV-1990 (Rel. 16, Last sequence update)  
15-DEC-1998 (Rel. 37, Last annotation update)  
Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).  
ADHA OR ADH1.  
Acetobacter aceti.  
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Acetobacteraceae; Acetobacter.  
NCBI\_TaxID=435;  
RN (1)  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-50.  
RP MEDLINE=89255070; PubMed=2722742;  
RX Inoue T., Sunagawa M., Mori A., Imai C., Fukuda M., Takagi M., Yano K.;  
"Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase subunit of alcohol dehydrogenase from Acetobacter aceti."  
J. Bacteriol. 171:3115-3122(1989).  
RN [2]  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE=9528964; PubMed=7772016;  
RA Cozier G.E., Giles I.G., Anthony C.;  
"The structure of the quinoprotein alcohol dehydrogenase of Acetobacter aceti modelled on that of methanol dehydrogenase from Methylobacterium extorquens."  
Biochem. J. 308:375-379(1995).  
CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde + reduced acceptor.  
CC -1- COFACTOR: POQ AND HEME.  
CC -1- SUBUNIT: TETRAMER OF NON IDENTICAL CHAINS (DEHYDROGENASE, CYTOCHROME, AND TWO SMALLER UNKNOWN SUBUNITS).  
CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.  
CC -1- SIMILARITY: Contains 1 cytochrome c domain.

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-----

CC EMBL; D90004; BAA14058.1; -  
CC PIR; J50326; J50326.  
CC HSSP; Q924J7; 1FLG.  
CC InterPro; IPR001479; Bac\_POQ.  
CC InterPro; IPR002372; Bac\_POQ\_repeat.  
CC InterPro; IPR000345; CytC\_heme\_bind.  
CC Pfam; PF01011; Bacterial\_POQ\_3.  
CC SMART; SM00564; POQ\_3.  
CC PROSITE; PS00363; BACTERIAL\_POQ\_1; 1.  
CC PROSITE; PS00364; BACTERIAL\_POQ\_2; 1.  
CC PROSITE; PS00190; CYTOCHROME\_C\_1.  
CC Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.  
CC SIGNAL 1 35  
CC CHAIN 36 742 ALCOHOL DEHYDROGENASE [ACCEPTOR].  
CC DOMAIN 633 742 CYTOCHROME C-LIKE.  
CC ACT\_SITE 343 343 BASE (POTENTIAL).  
CC BINDING 649 649 HEME (COVALENT) (BY SIMILARITY).

```

FT BINDING 652 652 HEME (COVALENT) (BY SIMILARITY).
FT METAL 653 653 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 742 AA, 81521 MW, 9C6C9268DAB825A CRC64;

Query Match
Best Local Similarity 70.0%; Score 34; DB 1; Length 742;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAYAMD 10
Db 684 RGALTRAYGMD 693

RESULT 8
DHET GLUTOX STANDARD; PRT: 757 AA.
AC 005542;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alchohol dehydrogenase [acceptor] precursor (EC 1.1.99.8) (G3-ADH subunit I).
GN ADHA.
OS Glucobacter oxydans (Glucobacter suboxydans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Glucobacter.
OX NCBI_TaxID=442;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-50.
RC STRAIN=IFO 12528; PubMed=9055427;
RA MEDLINE=97208225; PubMed=9055427;
RX Kondo K., Horinouchi S.;
RT "Characterization of the genes encoding the three-component membrane-bound alcohol dehydrogenase from Glucobacter suboxydans and their expression in Acetobacter pasteurianus."
RT Appl. Environ. Microbiol. 63:1131-1138(1997).
RL -1- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde + reduced acceptor.
CC -1- COFACTOR: POQ AND HEME.
CC -1- SUBUNIT: HETEROTRIMER (DEHYDROGENASE, CYTOCHROME AND PROTEIN ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC SPACE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
CC -1- SIMILARITY: Contains 1 cytochrome c domain.
-----
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-----
DR EMBL: D86375; BAA19753.1; -
DR HSSP: O9Z475; 1F1G.
DR InterPro: IPR001479; Bac_POQ.
DR InterPro: IPR002372; Bac_POQ_repeat.
DR InterPro: IPR000345; CytC_heme_bind.
DR Pfam: PF01011; Bacterial_POQ_4.
DR SMART: SM00564; POQ; 6.
DR PROSITE: PS00363; BACTERIAL_POQ_1; 1.
DR PROSITE: PS00364; BACTERIAL_POQ_2; 1.
DR PROSITE: PS00190; CYTOCHROME_C_1.
DR Oxidoreductase; POQ; Heme; Periplasmic; Membrane; signal;
KW Pyridoxal phosphate carboxylic acid.
FT CHAIN 1 34 ALCOHOL DEHYDROGENASE [ACCEPTOR].
FT DOMAIN 637 726 CYTOCHROME C-LIKE.
FT MOD_RES 35 35 PYRIDOXINE CARBOXYLIC ACID.
FT ACT_SITE 342 342 BASE (POTENTIAL).

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FT BINDING 653 653 HEME (COVALENT) (BY SIMILARITY).
FT METAL 656 656 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 757 AA, 82968 MW, 39B9F0E3B947581 CRC64;

Query Match
Best Local Similarity 70.0%; Score 34; DB 1; Length 757;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAYAMD 10
Db 688 RGALTRAYGMD 697

RESULT 9
DCML HYDPS STANDARD; PRT: 803 AA.
AC P1913; Q9R89;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L).
GN CUL.
OS Hydrogenophaga pseudoflava (Pseudomonas carboxydoflava).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Hydrogenophaga.
OX NCBI_TaxID=47421;
RN [1]
RP SEQUENCE FROM N.A., COFACTOR, AND SUBUNIT.
RA MEDLINE=99412255; PubMed=10482497;
RX Kang B.S., Kim Y.M.;
RT "Cloning and molecular characterization of the genes for carbon monoxide dehydrogenase and localization of molybdopterin, flavin adenine dinucleotide, and iron-sulfur centers in the enzyme of Hydrogenophaga pseudoflava."
RT J. Bacteriol. 181:5581-5590(1999).
RL [2]
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
RX MEDLINE=20425113; PubMed=10966817;
RA Haenzelmann P., Dobbek H., Gremer L., Huber R., Meyer O.;
RT "The effect of intracellular molybdenum in Hydrogenophaga pseudoflava on the crystallographic structure of the seleno-molybdo-iron-sulfur flavoenzyme carbon monoxide dehydrogenase."
RT J. Mol. Biol. 301:1221-1235(2000).
RL [4]
RN [5]
RP REVIEW.
RX MEDLINE=20525277; PubMed=11076018;
RA Meyer O., Gremer L., Ferner R., Ferner M., Dobbek H., Gnida M., Meyer-Klaucke W., Huber R.;
RT "The role of Se, Mo and Fe in the structure and function of carbon monoxide dehydrogenase."
RT J. Biol. Chem. 275:865-876(2000).
RL -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.
CC -1- COFACTOR: Molybdenum (molybdopterin).
CC -1- SUBUNIT: COMPOSED OF 2 HETEROTRIMERS. EACH HETEROTRIMER CONSISTS OF A LARGE, A MEDIUM AND A SMALL SUBUNIT. THE HETEROTRIMERS DIMERIZE TO FORM A HEXAMER.
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DR EMBL; U0806; AAD00363.1; -.

DR PIR; PLO139; PLO139.

DR PDB; 1FEV; 15-SEP-00.

DR PDB; 1FEV; 13-NOV-00.

DR Pfam; PF02738; Ald\_Xan\_dh\_C2; 1.

DR Pfam; PF01315; Ald\_Xan\_dh\_C; 1.

CC Oxidoreductase; Molybdenum; Selenium; Selenocysteine; 3D-structure.

FT SEQUENCE 803 AA; 87228 MW; 3CD5FE205DBE0712 CRC64;

QY Query Match 61.8%; Score 34; DB 1; Length 803;  
 Best Local Similarity 60.0%; Pred. No. 42;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSLTAYVMDY 11  
 : ||| :  
 302 ISTTAFARDY 311

RESULT 10  
 ID YFHM ECOLI STANDARD; PRT; 1653 AA.

AC P76578;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Hypothetical lipoprotein yfhm precursor.  
 GN YFHM OR B2520.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RT Science 277:1453-1474(1997).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 (Potential).

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CC -----  
 CC EMBL; AE000338; AAC75573.1; -.

DR PIR; G65028; G65028.

DR Ecocore; EGI3394; yfhm.

DR EMBL; U73857; AAB18118.1; ALT\_INIT.

DR EMBL; M64787; AAA23475.1; -.

DR PIR; B64768; B64768.

DR Ecocore; EGI2888; yafp.

DR InterPro; IPR000600; ROK\_family.

DR Pfam; PF00480; ROK; 1.

DR PROSITE; PS01125; ROK; 1.

CC Hypothetical protein; Complete proteome.

FT CHAIN 1 17 POTENTIAL.  
 FT DOMAIN 1559 1589 COILED COIL (POTENTIAL).  
 FT LIPID 18 18 N-ACYL DIGLYCERIDE (POTENTIAL).  
 SO SEQUENCE 1653 AA; 181584 MW; 13109EC5CDBA1A0 CRC64;

QY Query Match 61.8%; Score 34; DB 1; Length 1653;  
 Best Local Similarity 75.0%; Pred. No. 91;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYVMDY 11  
 : ||| :  
 Db 1253 LTRAYVMDY 1260

RESULT 11  
 ID YAFV ECOLI STANDARD; PRT; 302 AA.

AC P23917; P71316; P75705;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yafv.  
 GN YAFV OR B0394.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RA Ryder L., Sharples G.J., Lloyd R.G.;  
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RT Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,  
 RA Federspiel N., Hyman R., Kaiman S., Komp C., Kundi O., Lew H.,  
 RA Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 43-302 FROM N.A.  
 RX MEDLINE=92078081; PubMed=1744033;  
 RA Reeder T.C., Schleif R.F.;  
 RT "Mapping, sequence, and apparent lack of function of araJ, a gene of  
 RT the Escherichia coli arabinose regulon.";  
 RT J. Bacteriol. 173:7765-7771(1991).  
 CC -1- SIMILARITY: BELONGS TO THE ROK (NAGC/XYLR) FAMILY. STRONG, TO  
 CC H. INFLUENZAE HI0182.

CC -----  
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CC -----  
 CC EMBL; X76979; CAA54284.1; -.

DR EMBL; AE000145; AAC73497.1; ALT\_INIT.

DR EMBL; U73857; AAB18118.1; ALT\_INIT.

DR EMBL; M64787; AAA23475.1; -.

DR PIR; B64768; B64768.

DR Ecocore; EGI2888; yafp.

DR InterPro; IPR000600; ROK\_family.

DR Pfam; PF00480; ROK; 1.

DR PROSITE; PS01125; ROK; 1.

CC Hypothetical protein; Complete proteome.

FT CHAIN 1 17 POTENTIAL.  
 FT DOMAIN 1559 1589 COILED COIL (POTENTIAL).  
 FT LIPID 18 18 N-ACYL DIGLYCERIDE (POTENTIAL).  
 SO SEQUENCE 302 AA; 32500 MW; 9791F9C29C91049C CRC64;

QY Query Match 60.0%; Score 33; DB 1; Length 302;  
 Best Local Similarity 60.0%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



QY 2 VSITAYAMDY 11  
 DB 188 ISCTGFAMDY 197

RESULT 12  
 ID PANK1\_MOUSE STANDARD; PRT; 548 AA.  
 AC Q8K4K6; Q9D3K1; Q9QXW8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase 1)  
 GN (PANK1 OR PANK).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;

(1)  
 SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
 MEDLINE=20092916; PubMed=1062568;  
 Rock C.O., Calder R.B., Karim M.A., Jackowski S.;  
 "Pantothenate kinase regulation of the intracellular concentration of  
 coenzyme A.";  
 J. Biol. Chem. 275:1377-1383 (2000).  
 [2]  
 SEQUENCE FROM N.A. (ISOFORM 1), CHARACTERIZATION, AND ALTERNATIVE  
 SPLICING.  
 MEDLINE=22090536; PubMed=12095677;  
 Rock C.O., Karim M.A., Zhang Y.M., Jackowski S.;  
 "The murine pantothenate kinase (Pank1) gene encodes two  
 differentially regulated pantothenate kinase isozymes.";  
 Gene 291:35-43 (2002).  
 [3]  
 SEQUENCE FROM N.A. (ISOFORM 1).  
 STRAIN=C57BL/6J; TISSUE=Head;  
 MEDLINE=21085660; PubMed=1217851;  
 Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Batsch G.,  
 Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Norone P., Ring B., Rindowbach C., Seta T., Shizata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,  
 Hayashizaki Y.;  
 "Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409:685-690 (2001).  
 [4]  
 SEQUENCE FROM N.A. (ISOFORM 2).  
 TISSUE=Liver, and Skeletal muscle;  
 MEDLINE=22388257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Umedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mollahy S.J.,  
 Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.T., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL FUNCTION: Plays a role in the physiological regulation of the  
 intracellular CoA concentration.  
 CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-  
 phosphopantothenate.  
 CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its  
 thioesters. Strongly inhibited by acetyl-CoA and by many CoA and  
 also inhibited by high concentration of non-esterified CoA  
 (CoASH). Isoform 1 is inhibited by high concentration of non-  
 esterified CoA (CoASH) and strongly inhibited by acetyl-CoA and by  
 malonyl-CoA. Isoform 2 is stimulated by CoA and weakly inhibited  
 by acetyl-CoA and malonyl-CoA.  
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Pank1-alpha;  
 CC IsoId=Q8K4K6-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Pank1-beta;  
 CC IsoId=Q8K4K6-2; Sequence=VSP 004522, VSP 004523;  
 CC -1- TISSUE SPECIFICITY: Expressed in liver and kidney. Isoform 1 is  
 highly expressed in heart and skeletal muscle, whereas isoform 2  
 is expressed exclusively in testis.  
 CC -1- DOMAIN: The N-terminal extension, present in isoform 1 may be the  
 regulatory domain.  
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL; AF200357; AAF2952.1; -  
 CC DR EMBL; AF347700; AAM77216.1; -  
 CC DR EMBL; AK017345; BAB30700.1; -  
 CC DR EMBL; BC023466; AAH23496.1; -  
 CC DR MGD; MGI:1922985; Pank1.  
 CC GO; GO:0004594; F:pantothenate kinase activity; IDA.  
 CC DR InterPro; IPR004567; Pank\_eukar.  
 CC DR Pfam; PF03630; Pumble; 1.  
 CC KW Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis;  
 CC KW Alternative splicing  
 CC FT VARSPPLIC 1 175 Missing (in isoform 2).  
 CC FT FTID=VSP 004522.  
 CC FT FT MDSGRKNRP -> MKLVNGRKQT (in isoform 2).  
 CC FT FT /FTID=VSP 004523.  
 CC FT FT  
 CC SO SEQUENCE 548 AA; 60091 MW; C916709D048E829B CRC64;

QY 2 VSITAYAMDY 11  
 DB 506 MKLVNAMDY 515

RESULT 13  
 ID PANK2\_HUMAN STANDARD; PRT; 570 AA.  
 AC Q9B2Z3; Q8N7Q4; Q8TCK5; Q9BYW5; Q9HAF2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

Query Match 60.0%; Score 33; DB 1; Length 548;  
 Best Local Similarity 60.0%; Pred. No. 46;  
 Matches 6; Conservative 2; Mismatches 0; Gaps 0;

DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Pantothenate kinase 2, mitochondrial precursor (EC 2.7.1.33)  
 GN PANK2 OR C20ORF48.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteletia; Primates; Catarrhini; Homindae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION.  
 RC TISSUE=Brain;  
 RX PubMed=12554685;  
 RA Hoernagel K., Prokisch H., Meltinger T.;  
 RT "An isoform of hPANK2, deficient in pantothenate kinase-associated  
 RT neurodegeneration, localizes to mitochondria."  
 RL Hum. Mol. Genet. 12:321-327(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.W., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Cowley G.J., Dedman R., Dhali P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,  
 RA Garmham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hamblin D.V., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leheslahti M.H., Leverhulme M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McCombs L.J., McLay K., McMurtry A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,  
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showken R., Sims S.,  
 RA Sruce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilmink L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20."  
 RL Nature 414:865-871(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANT GLY-126.  
 RC TISSUE=Testis;  
 RX Suzuki O., Sasaki N., Aotaka S., Shoji T., Ichihara T., Shiohata N.,  
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,  
 RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,  
 RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Katoka R.,  
 RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,  
 RA Matsunabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,  
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
 RA Kikuma K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,  
 RA Kikuchi H., Kanda K., Wagauma M., Murakawa K., Kanehori K.,  
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,  
 RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T., Ota T.,  
 RA Hayashi K., Hara H., Tanase T., Nomura Y., Togiya S., Komai F.,  
 RA Hara R., Takeuchi K., Arita M., Nabekura T., Kawai Y.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 406-570 FROM N.A.  
 RC TISSUE=Brain;  
 RX Koehler K., Beyer A., Mewes H.-W., Weil B., Wiemann S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP DISEASE.  
 RX MEDLINE=22053542; PubMed=12058097;  
 RA Ching K.H.L., Westaway S.K., Gitschier J., Higgins J.J.,

RA Hayflick S.J.;  
 RT "HAP syndrome is allelic with pantothenate kinase-associated  
 RT neurodegeneration."  
 RL Neurology 58:1673-1674(2002).  
 RN [6]  
 RP VARIANTS GLN-111 AND GLY-126, VARIANTS PRAN VAL-219; ALA-234; TRP-264;  
 RP CYS-278; VAL-282; CYS-286; ILE-327; PRO-351; SER-355; ILE-404;  
 RP PRO-413; ASN-471; TRP-497; ILE-500; ARG-521 AND MET-528, AND TISSUE  
 RP SPECIFICITY.  
 RX MEDLINE=21372465; PubMed=11479594;  
 RA Zhou B., Westaway S.K., Levinson B., Johnson M.A., Gitschier J.,  
 RA Hayflick S.J.;  
 RT "A novel pantothenate kinase gene (PANK2) is defective in  
 RT Hallervorden-Spatz syndrome."  
 RL Nat. Genet. 28:345-349(2001).  
 CC -1- FUNCTION: Maybe the master regulator of the CoA biosynthesis (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-  
 CC phosphopantothenate.  
 CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its  
 CC thioesters.  
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and mitochondrial.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9B23-1; Sequence=Displayed;  
 CC Note=Mitochondrial isoform;  
 CC Name=3;  
 CC IsoId=Q9B23-2; Sequence=VSP\_007424;  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, 1 (shown here) and 2, are produced by  
 CC alternative initiation;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous.  
 CC -1- DISEASE: Defects in PANK2 are the cause of pantothenate kinase-  
 CC associated neurodegeneration (PKAN) [MIM:234200], formerly known  
 CC as Hallervorden-Spatz syndrome (HSS). PKAN is an autosomal  
 CC recessive neurodegenerative disorder associated with iron  
 CC accumulation in the brain. Clinical features include  
 CC extrapyramidal dysfunction, and a relentlessly progressive course.  
 CC Atypical PKAN is diagnosed in individuals who may not fit with the  
 CC diagnostic criteria of PKAN yet have radiographic or pathologic  
 CC evidence of increased basal ganglia iron.  
 CC -1- DISEASE: Defects in PANK2 are the cause of  
 CC hypoparathyroidism, acanthocytosis, retinitis pigmentosa,  
 CC and pallidal degeneration (HARP) [MIM:607236]. HARP is a rare  
 CC syndrome with many clinical similarities to PKAN.  
 CC -1- MISCELLANEOUS: The HSS syndrome has been proposed to  
 CC and Hugo Spatz during World War II.  
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC -1- CAUTION: In addition to the presence of a second start site in  
 CC position 124, it is not excluded that the Leu-111 may  
 CC exceptionally also serve as an alternative initiation codon.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF94409; AAN32907.1; -;  
 CC EMBL; AL353194; CAC15924.2; ALT\_SEQ.  
 CC EMBL; AL031670; CAC32829.1; -;  
 CC EMBL; AK021791; BAB13897.1; -;  
 CC EMBL; AK097796; BAC05173.1; ALT\_INIT.  
 CC EMBL; AL713654; CAD28463.1; -;  
 CC Genew; HGNC:15894; PANK2.  
 CC DR MIM; 606157; -;

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DR MIM; 234200; -
DR MIM; 607236; -
DR InterPro; IPR004567; Pank_eukar.
DR Pfam; PF03630; Fumble; 1.
KW Transferrase; kinase; ATP-binding; Coenzyme A biosynthesis;
KW Alternative splicing; Alternative initiation; transit peptide;
FT TRANSIT 1 46 MITOCHONDRION (POTENTIAL).
FT CHAIN 47 570 PANTOTHENATE KINASE 2, ISOFORM 1.
FT INIT MET 124 570 PANTOTHENATE KINASE 2, ISOFORM 2.
FT DOMAIN 236 243 FOR ISOFORM 2.
FT VARSPLIC 1 291 POLY-GLU.
FT VARIANT 111 111 Missing (in isoform 3).
FT VARIANT 126 126 /FTId=VSP_007424.
FT VARIANT 126 126 L -> O.
FT VARIANT 219 219 /FTId=VAR_015152.
FT VARIANT 219 219 A -> G.
FT VARIANT 234 234 /FTId=VAR_015153.
FT VARIANT 234 234 G -> V (in PRAN; atypical).
FT VARIANT 264 264 /FTId=VAR_015154.
FT VARIANT 264 264 T -> A (in PRAN; atypical).
FT VARIANT 264 264 /FTId=VAR_015155.
FT VARIANT 264 264 R -> W (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015156.
FT VARIANT 264 264 R -> C (in PRAN; atypical).
FT VARIANT 264 264 /FTId=VAR_015157.
FT VARIANT 264 264 L -> V (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015158.
FT VARIANT 264 264 R -> C (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015159.
FT VARIANT 264 264 T -> I (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015160.
FT VARIANT 264 264 S -> P (in PRAN; atypical).
FT VARIANT 264 264 /FTId=VAR_015161.
FT VARIANT 264 264 N -> S (in PRAN; atypical).
FT VARIANT 264 264 /FTId=VAR_015162.
FT VARIANT 264 264 N -> I (in PRAN; atypical).
FT VARIANT 264 264 /FTId=VAR_015163.
FT VARIANT 264 264 L -> P (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015164.
FT VARIANT 264 264 S -> N (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015165.
FT VARIANT 264 264 I -> T (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015166.
FT VARIANT 264 264 N -> I (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015167.
FT VARIANT 264 264 G -> R (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015168.
FT VARIANT 264 264 T -> M (in PRAN).
FT VARIANT 264 264 /FTId=VAR_015169.

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Query Match 60.0%; Score 33; DB 1; Length 570;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 4 LTYVANDY 11
| | | | |
Db 533 LLAAYALDY 540

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RESULT 14
PANK1_HUMAN STANDARD; PRT; 598 AA.
AC 08TEB04: 08TEB08:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase 1)
DE (hPank1) (hPank).
GN PANK1 OR PANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Fetal brain;
RX MEDLINE=21668246; PubMed=11809413;
RA Ni X., Ma Y., Cheng H., Jiang M., Ying K., Xie Y., Mao Y.;
RT "Cloning and characterization of a novel human pantothenate kinase
gene."
RL Int. J. Biochem. Cell Biol. 34:109-115(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 460-598 FROM N.A. (ISOFORM 2).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usetin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalski U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP IDENTIFICATION OF ISOFORM 1.
RA Zhou B., Westway S.K., Levinson B., Johnson M.A., Gitschler J.,
RA Hayflick S.J.;
RL Unpublished observations (JUL-2001).
CC -!- FUNCTION: Plays a role in the physiological regulation of the
CC intracellular CoA concentration (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -!- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
CC thioesters. Strongly inhibited by acetyl-CoA and by many CoA and
CC also inhibited by high concentration of non-esterified CoA (CoASH)
CC (By similarity).
CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Pank1-alpha;
CC IsoId=Q8TEB04-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8TEB04-2; Sequence=VSP_004520;
CC Name=3;
CC IsoId=Q8TEB04-3; Sequence=VSP_004521;
CC -!- TISSUE SPECIFICITY: Expressed in liver and kidney.
CC -!- DOMAIN: The N-terminal extension, present in isoform 1 may be the
CC regulatory domain.
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
CC -!- CAUTION: Isoform 2, although confirmed in the murine ortholog, is
CC only partially cloned and needs a further complete identification.
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:38:22 ; Search time 14.85 Seconds  
(without alignments)  
71.236 Million cell updates/sec

Title: US-09-759-112a-19  
Perfect score: 55  
Sequence: 1 RVSLTRYAMDY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:.\*  
1: pirl:.\*  
2: pirl2:.\*  
3: pirl3:.\*  
4: pirl4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	69.1	106	2	Ig heavy chain V r
2	38	69.1	1644	2	probable lipoprote
3	37	67.3	190	2	hypothetical prote
4	35	63.6	345	2	probable oxidoredu
5	34	61.8	314	2	conserved hypothet
6	34	61.8	388	2	alanine racemase B
7	34	61.8	599	2	hypothetical prote
8	34	61.8	738	2	alcohol dehydrogen
9	34	61.8	742	2	alcohol dehydrogen
10	34	61.8	742	2	alcohol dehydrogen
11	34	61.8	1653	2	hypothetical prote
12	34	61.8	1653	2	hypothetical prote
13	34	61.8	1653	2	hypothetical prote
14	34	61.8	1653	2	hypothetical prote
15	34	61.8	1653	2	hypothetical prote
16	34	61.8	1653	2	hypothetical prote
17	34	61.8	1653	2	hypothetical prote
18	34	61.8	1653	2	hypothetical prote
19	34	61.8	1653	2	hypothetical prote
20	34	61.8	1653	2	hypothetical prote
21	34	61.8	1653	2	hypothetical prote
22	34	61.8	1653	2	hypothetical prote
23	34	61.8	1653	2	hypothetical prote
24	34	61.8	1653	2	hypothetical prote
25	34	61.8	1653	2	hypothetical prote
26	34	61.8	1653	2	hypothetical prote
27	34	61.8	1653	2	hypothetical prote
28	34	61.8	1653	2	hypothetical prote
29	34	61.8	1653	2	hypothetical prote

30	32	58.2	289	2	B69217	hypothetical prote
31	32	58.2	329	2	D86733	hypothetical prote
32	32	58.2	334	2	AH1497	transcription regu
33	32	58.2	334	2	A11139	transcription regu
34	32	58.2	454	2	T50193	probable seryl-trn
35	32	58.2	480	2	B90012	hypothetical prote
36	32	58.2	519	2	AB3449	xanthine dehydroge
37	32	58.2	531	2	B83422	probable serine/th
38	32	58.2	676	2	E72662	hypothetical prote
39	32	58.2	944	2	S69679	hypothetical prote
40	32	58.2	986	1	A23646	invasin - Yersinia
41	32	58.2	1025	2	H86250	hypothetical prote
42	32	58.2	1048	2	T18334	icmB protein - Leg
43	32	58.2	1230	2	T07663	soluble starch syn
44	31	56.4	111	2	PH0992	Ig heavy chain V r
45	31	56.4	134	2	F64817	probable membrane

## ALIGNMENTS

## RESULT 1

S26315  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26315  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26315  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-106 <STA>  
A:Cross-references: EMBL:X59208; NID:952079; PIDN:CAA41918.1; PID:G1334042  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:2-85/Domain: immunoglobulin homology <IMW>

Query Match 69.1%; Score 38; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAYAMDY 11  
Db 89 TAYAMDY 95

## RESULT 2

AC0823  
probable lipoprotein STY2778 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AC0823  
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T. J.; Comerford, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
C:Accession: AC0823  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1644 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD02735.1; PID:G16503746; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2778  
Query Match 69.1%; Score 38; DB 2; Length 1644;  
Best Local Similarity 87.5%; Pred. No. 30;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LTVAYMDY 11  
 |||||:  
 Db 1245 LTVAYMDF 1252

RESULT 3  
 T46408  
 hypothetical protein DKFZp434E172.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C/Accession: T46408  
 R:Blum, H.; Bauerbach, S.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: 223034  
 A:Accession: T46408  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Idgenes: 1-190 <AAA>  
 A:Cross-references: EMBL:AL137464  
 A:Experimental source: adult testis; clone DKFZp434E1722  
 C:Genetics:

A:Note: DKFZp434E172.1

Query Match 67.3%; Score 37; DB 2; Length 190;  
 Best Local Similarity 54.5%; Pred. No. 5.4;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLTAYAMD 11  
 ::|||:::  
 Db 127 KMSLNAYALDF 137

RESULT 4  
 T35266  
 probable oxidoreductase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
 C/Accession: T35266  
 R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, April 1999  
 A:Reference number: 221573  
 A:Accession: T35266  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-345 <DLI>  
 A:Cross-references: EMBL:AL049587; PIDN:CA840691.1; GSPDB:GN00070; SCOEDB:SCSF2A.24  
 A:Experimental source: strain A3(2)  
 A:Genetics:

A:Gene: SCOEDB:SCSF2A.24

Query Match 63.6%; Score 35; DB 2; Length 345;  
 Best Local Similarity 70.0%; Pred. No. 25;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAYAMD 10  
 |||||:  
 Db 280 RVRLTAYRLD 289

RESULT 5  
 G96020  
 conserved hypothetical exported protein Smb20724 [imported] - Sinorhizobium meliloti (str  
 C:Species: Sinorhizobium meliloti  
 C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C/Accession: G96020  
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A>Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo  
 A:Reference number: A95842; MUID:2136508; PMID:1181431  
 A:Accession: G96020  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-314 <KUR>  
 A:Cross-references: GB:AL591985; PIDN:CA649831.1; PID:g15141319; GSPDB:GN00167  
 A:Experimental source: strain 1021, megaplasmid pSymB  
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Anpe, F.; Barloy-Hubler,  
 Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kles, E.; Komp, C.; Lelaure,  
 hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K  
 A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: Smb20724  
 A:Genome: plasmid

Query Match 61.8%; Score 34; DB 2; Length 314;  
 Best Local Similarity 60.0%; Pred. No. 37;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSLTAYAMDY 11  
 ::|||:::  
 Db 14 IALPAYADY 23

RESULT 6  
 H83714  
 alanine racemase BH0520 [imported] - Bacillus halodurans (strain C-125)  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C/Accession: H83714  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Accession: H83714  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-388 <STO>  
 A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04239.1; GSPDB:GN00  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH0520  
 C:Superfamily: alanine racemase

Query Match 61.8%; Score 34; DB 2; Length 388;  
 Best Local Similarity 45.5%; Pred. No. 46;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAYAMDY 11  
 ::|||:::  
 Db 101 RITLTAYQLDW 111

RESULT 7  
 S46630  
 hypothetical protein YJL201w - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: hypothetical protein J0325  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 29-Oct-1999  
 C/Accession: S46630; S30800; S56988  
 R:Purnelle, B.; Cosser, F.; Goffeau, A.  
 Yeast 10, 1235-1249, 1994  
 A>Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies  
 ase gene ACO1 and two homologues to chromosome III genes.  
 A:Reference number: S46621; MUID:95274326; PMID:7754713  
 A:Accession: S46630  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-539 <PUR>  
 A:Cross-references: EMBL:X77688; NID:g1183992; PIDN:CA454756.1; PID:G547591  
 R:Arnas, J.E.; Abelson, J.N.

submitted to the EMBL Data Library, December 1992  
A:Description: The Saccharomyces cerevisiae PRP21 gene product is required for pre-spliced  
A:Reference number: S30799  
A:Accession: S30800  
A:Molecule type: DNA  
A:Residues: 1-333 <ARE>  
A:Cross-references: EMBL:L07744; NID:g172275; PIDN:AAB09602.1; PID:g402334  
R:Purille, B.; Coster, F.; Goffeau, A.  
submitted to the Protein Sequence Database, September 1995  
A:Reference number: S56977  
A:Accession: S56988  
A:Molecule type: DNA  
A:Residues: 1-599 <PUW>  
A:Cross-references: EMBL:249476; NID:g1008420; PIDN:CAA89496.1; PID:g1008421; MIPS:YUL20  
C:Genetics:  
A:Gene: SGD:ECM25  
A:Cross-references: SGD:S0003737; MIPS:YUL201w  
A:Map position: 10L

Query Match  
Best Local Similarity 61.8%; Score 34; DB 2; Length 599;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMDY 11  
Db 157 R1SLNVLXYDY 167

RESULT 8  
S14270  
alcohol dehydrogenase, membrane-bound (EC 1.1.-.-) 72k chain precursor - Acetobacter pol  
C:Species: Acetobacter polyoxogenes  
A:Variety: strain NB11028  
C:Date: 21-Nov-1993 #sequence\_revision 26-Jul-1996 #text\_change 20-Jun-2000  
C:Accession: S14270  
R:Tanaka, T.; Fukaya, M.; Takemura, H.; Tayama, K.; Okumura, H.; Kawamura, Y.; Nishiyama  
Biochim. Biophys. Acta 1088, 292-300, 1991  
A:Title: Cloning and sequencing of the gene cluster encoding two subunits of membrane-bc  
A:Reference number: S14270; MUID:91159482; PMID:2001402  
A:Accession: S14270  
A:Molecule type: DNA  
A:Residues: 1-738 <TAM>  
A:Cross-references: GB:D00635; NID:g216185; PIDN:BAA00528.1; PID:g216186  
A:Experimental source: strain NB11028  
C:Complex: heterodimer of 72k and 44k chains  
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)  
C:Keywords: alcohol metabolism; membrane protein; oxidoreductase  
C:Domain: signal sequence #status predicted <Sig>  
C:Product: alcohol dehydrogenase 72k chain #status predicted <MAT>

Query Match  
Best Local Similarity 61.8%; Score 34; DB 2; Length 738;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMD 10  
Db 685 RGALTRAYGMD 694

RESULT 9  
J50326  
alcohol dehydrogenase (EC 1.1.-.-) 72k chain precursor - Acetobacter acet  
C:Species: Acetobacter acet  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 20-Jun-2000  
C:Accession: J50326  
R:Inoue, T.; Sunagawa, M.; Mori, A.; Inai, C.; Fukuda, M.; Takagi, M.; Yano, K.  
J. Bacteriol. 171, 3115-3122, 1989  
A:Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase sub  
A:Reference number: J50326; MUID:89255070; PMID:2722742  
A:Accession: J50326  
A:Molecule type: DNA  
A:Residues: 1-742 <INO>  
A:Cross-references: GB:D90004; GB:M26951; NID:g216193; PIDN:BAA14058.1; PID:g216194

A:Experimental source: strain K6033  
A>Note: amino terminal of mature protein is confirmed  
C:Genetics:  
A:Gene: adh1  
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)  
C:Keywords: alcohol metabolism; NAD; oxidoreductase  
F:1-35/Domain: signal sequence #status predicted <Sig>  
F:36-742/Product: alcohol dehydrogenase 72k dehydrogenase chain #status predicted <ADC>

Query Match  
Best Local Similarity 61.8%; Score 34; DB 2; Length 742;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMD 10  
Db 684 RGALTRAYGMD 693

RESULT 10  
A49340  
alcohol dehydrogenase (EC 1.1.-.-) precursor - Acetobacter pasteurianus (strain NC11380)  
C:Species: Acetobacter pasteurianus  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Jun-2000  
C:Accession: A49340  
R:Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T.  
J. Bacteriol. 175, 6857-6866, 1993  
A:Title: Induction by ethanol of alcohol dehydrogenase activity in Acetobacter pasteuria  
A:Reference number: A49340; MUID:94042848; PMID:8226628  
A:Accession: A49340  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-742 <TAK>  
A:Cross-references: GB:D13893; NID:g517067; PIDN:BAA40252.1; PID:g452586  
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)  
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match  
Best Local Similarity 61.8%; Score 34; DB 2; Length 742;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMD 10  
Db 684 RGALTRAYGMD 693

RESULT 11  
B91052  
hypothetical protein ECs3386 [imported] - Escherichia coli (strain O157:H7, substrain RI  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: B91052  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gesawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: B91052  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1653 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA836809.1; PID:g13362856; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECs3386

Query Match  
Best Local Similarity 61.8%; Score 34; DB 2; Length 1653;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYAMDY 11  
Db 1253 LTRAYVMDR 1260

## RESULT 12

P85896

hypothetical protein 23787 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C:Species: Escherichia coli

C&gt;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: F85896

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; DiMantano, E.; Potamousta, K.; Apodaca,

Nature 409 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85896

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1653 &lt;GTO&gt;

A:Cross-references: GB:AE005174; NID:G12516921; PIDN:AA657634.1; GSPDB:GN00145; UMGF:237

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

Query Match

Best Local Similarity 61.8%; Score 34; DB 2; Length 1653;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTAYAMDY 11

DB 1253 LTAYVMDP 1260

## RESULT 13

G65028

hypothetical protein b2520 - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C&gt;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002

C:Accession: G65028

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A:Rose, D.J.; Mau, B.; Sha, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G65028

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1653 &lt;BLAT&gt;

A:Cross-references: GB:AE000338; GB:U00096; NID:G1788862; PIDN:AA675573.1; PID:G1788868;

A:Experimental source: strain K-12, substrain MG1655

Query Match

Best Local Similarity 61.8%; Score 34; DB 2; Length 1653;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTAYAMDY 11

DB 1253 LTAYVMDP 1260

## RESULT 14

S32786

Ig heavy chain (anti-biotin) - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S32786

R:Bagci, H.; Kohen, F.; Kucunoglu, U.; Bayer, E.A.; Wiltchek, M.

FEBS Lett. 322, 47-50, 1993

A:Title: Monoclonal anti-biotin antibodies simulate avidin in the recognition of biotin.

A:Reference number: S32786; MUID:93245957; PMID:8482366

A:Accession: S32786

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-118 &lt;BAG&gt;

A:Cross-references: GB:S59639; NID:G299965; PIDN:AA626438.1; PID:G299966

C:Superfamily: immunoglobulin V region, immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 60.0%; Score 33; DB 2; Length 118;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLTAYAMDY 11

DB 28 SLTAYGVDV 36

## RESULT 15

B53285

Ig heavy chain V and J regions, monoclonal antibody OHP101.B11.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C:Accession: B53285

R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struc

and their pH-reactivity profiles.

A:Reference number: A53285; MUID:92017897; PMID:1922102

A:Accession: B53285

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Note: sequence inconsistent with nucleotide translation

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 60.0%; Score 33; DB 2; Length 119;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVSILTAYAMDY 11

DB 98 RGLRLRYAMDY 108

Search completed: September 10, 2003, 17:42:42  
Job time: 16.85 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:42:07 ; Search time 22 Seconds  
(without alignments)  
72.956 Million cell updates/sec

Title: US-09-759-112a-19  
Perfect score: 55  
Sequence: 1 RVSLTRYAMDY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	11	11	US-09-759-112a-19
2	55	100.0	121	11	US-09-759-112a-7
3	55	100.0	139	15	US-10-156-761-9210
4	34	61.8	130	9	US-09-802-077-5
5	34	61.8	130	9	US-09-802-096-5
6	34	61.8	130	11	US-09-925-179-5
7	34	61.8	249	9	US-09-730-374-3
8	34	61.8	1046	15	US-10-128-714-3288
9	34	61.8	1199	15	US-10-128-714-8288
10	34	61.8	1653	9	US-09-741-669-402
11	33	60.0	16	11	US-09-880-748-2309
12	33	60.0	130	9	US-09-925-299-999
13	33	60.0	130	11	US-09-925-299-999
14	33	60.0	251	11	US-09-880-748-231
15	33	60.0	329	12	US-10-238-075-368

16	33	60.0	604	12	US-10-303-664A-57	Sequence 57, Appl
17	33	60.0	687	12	US-10-181-319-2	Sequence 2, Appl
18	33	60.0	1010	12	US-10-238-075-945	Sequence 945, Ap
19	32	58.2	16	11	US-09-880-748-2253	Sequence 2253, Ap
20	32	58.2	147	9	US-09-797-481-4	Sequence 4, Appl
21	32	58.2	147	9	US-09-844-736-6	Sequence 6, Appl
22	32	58.2	147	15	US-10-162-396-6	Sequence 6, Appl
23	32	58.2	181	15	US-10-156-761-10043	Sequence 10043, A
24	32	58.2	251	11	US-09-880-748-237	Sequence 237, Ap
25	32	58.2	264	15	US-10-167-015-12	Sequence 12, Appl
26	32	58.2	326	9	US-09-943-002-4	Sequence 4, Appl
27	32	58.2	409	15	US-10-156-761-11450	Sequence 11450, A
28	32	58.2	602	15	US-10-156-761-10462	Sequence 10462, A
29	32	58.2	677	15	US-10-284-668-2	Sequence 2, Appl
30	32	58.2	986	10	US-09-870-759-33	Sequence 33, Appl
31	32	58.2	986	12	US-09-751-108A-33	Sequence 33, Appl
32	32	58.2	1197	15	US-10-284-668-12	Sequence 12, Appl
33	31	56.4	16	11	US-09-880-748-2244	Sequence 2244, Ap
34	31	56.4	66	11	US-09-764-891-4633	Sequence 4633, Ap
35	31	56.4	196	10	US-09-764-864-1137	Sequence 1137, Ap
36	31	56.4	251	11	US-09-880-748-92	Sequence 92, Appl
37	31	56.4	268	11	US-09-557-796-21	Sequence 21, Appl
38	31	56.4	303	10	US-09-866-572A-20	Sequence 20, Appl
39	31	56.4	303	10	US-09-866-570A-20	Sequence 20, Appl
40	31	56.4	303	15	US-10-166-984-20	Sequence 20, Appl
41	31	56.4	340	9	US-09-775-195-2	Sequence 2, Appl
42	31	56.4	340	9	US-09-775-195-5	Sequence 5, Appl
43	31	56.4	340	9	US-09-775-195-6	Sequence 6, Appl
44	31	56.4	340	15	US-10-155-947-2	Sequence 2, Appl
45	31	56.4	340	15	US-10-155-947-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-759-112a-19  
; Sequence 19, Application US/09759112A  
; Publication No. US20030100741A1  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Sybille  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 200-013  
; CURRENT APPLICATION NUMBER: US/09/759, 112A  
; CURRENT FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 19  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-759-112a-19

Query Match 100.0%; Score 55; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVSLTRYAMDY 11  
DB 1 RVSLTRYAMDY 11

RESULT 2  
US-09-759-112a-7  
; Sequence 7, Application US/09759112A  
; Publication No. US20030100741A1  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT

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; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-09-759-112A-7

Query Match
Best Local Similarity 100.0%; Score 55; DB 11; Length 121;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVSLEYAYMDY 11
100 RVSLEYAYMDY 110

RESULT 3
US-10-156-761-9210
; Sequence 9210, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRU
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9210
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Streptomyces avermectilis
US-10-156-761-9210

Query Match
Best Local Similarity 63.6%; Score 35; DB 15; Length 339;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLEYAYMDY 10
280 RVSLEYAYMDY 289

RESULT 4
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
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; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Query Match
Best Local Similarity 61.8%; Score 34; DB 9; Length 130;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYAMDY 11
99 VVAYAMDY 106

RESULT 5
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Query Match
Best Local Similarity 75.0%; Score 32; DB 9; Length 130;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYAMDY 11
99 VVAYAMDY 106

RESULT 6
US-09-925-179-5
; Sequence 5, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-19E Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
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;; PRIOR FILING DATE: 1995-03-15  
;; PRIOR APPLICATION NUMBER: US 08/185,899  
;; PRIOR FILING DATE: 1994-01-26  
;; PRIOR APPLICATION NUMBER: PCT/US92/06860  
;; PRIOR FILING DATE: 1992-08-14  
;; PRIOR APPLICATION NUMBER: US 07/879,495  
;; PRIOR FILING DATE: 1992-05-07  
;; PRIOR APPLICATION NUMBER: US 07/744,768  
;; PRIOR FILING DATE: 1991-08-14  
;; NUMBER OF SEQ ID NOS: 68  
;; SEQ ID NO 5  
;; LENGTH: 130  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-925-179-5

Query Match 61.8%; Score 34; DB 11; Length 130;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

4 LTAYAMDY 11  
:|||||  
99 VVAYAMDY 106

RESULT 7  
US-09-730-374-3  
;; Sequence 3, Application US/09730374  
;; Patent No. US20010031261A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lust, John A.  
;; APPLICANT: Donovan, Kathleen A.  
;; TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES  
;; TITLE OF INVENTION: TO CD38 TO TREAT MULTIPLE MYELOMA  
;; FILE REFERENCE: 150,188US2  
;; CURRENT FILING DATE: 2001-05-10  
;; PRIOR FILING DATE: 2001-05-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/12512  
;; PRIOR FILING DATE: 1999-06-04  
;; PRIOR APPLICATION NUMBER: 60/088,277  
;; PRIOR FILING DATE: 1998-08-05  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 249  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: A polypeptide encoded by an open reading frame of  
;; OTHER INFORMATION: SEQ ID NO:1  
US-09-730-374-3

Query Match 61.8%; Score 34; DB 9; Length 249;  
Best Local Similarity 85.7%; Pred. No. 64;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

5 TAYAMDY 11  
:|||||  
108 TGYAMDY 114

RESULT 8  
US-10-128-714-3288  
;; Sequence 3288, Application US/10128714  
;; Publication No. US20030119013A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jiang, Bo  
;; APPLICANT: Hu, Weng  
;; APPLICANT: Tishkoff, Daniel  
;; APPLICANT: Zamudio, Carlos  
;; APPLICANT: Eroshkin, Alexey M  
;; APPLICANT: Lemieux, Sebastien M  
;; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

;; TITLE OF INVENTION: Methods of Use  
;; FILE REFERENCE: 10182-018-999  
;; CURRENT APPLICATION NUMBER: US/10/128,714  
;; CURRENT FILING DATE: 2002-04-23  
;; PRIOR APPLICATION NUMBER: US 60/285,697  
;; PRIOR FILING DATE: 2001-04-23  
;; PRIOR APPLICATION NUMBER: US 60/287,066  
;; PRIOR FILING DATE: 2001-04-27  
;; PRIOR APPLICATION NUMBER: US 60/295,890  
;; PRIOR FILING DATE: 2001-06-05  
;; PRIOR APPLICATION NUMBER: US 60/303,899  
;; PRIOR FILING DATE: 2001-07-09  
;; PRIOR APPLICATION NUMBER: US 60/316,362  
;; PRIOR FILING DATE: 2001-08-31  
;; NUMBER OF SEQ ID NOS: 8603  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 3288  
;; LENGTH: 1046  
;; TYPE: PRT  
;; ORGANISM: Aspergillus fumigatus  
US-10-128-714-3288

Query Match 61.8%; Score 34; DB 15; Length 1046;  
Best Local Similarity 66.7%; Pred. No. 3e+02;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

2 VSLTAYAMD 10  
:|||||  
69 MSLTSYSMD 77

RESULT 9  
US-10-128-714-8288  
;; Sequence 8288, Application US/10128714  
;; Publication No. US20030119013A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jiang, Bo  
;; APPLICANT: Hu, Weng  
;; APPLICANT: Tishkoff, Daniel  
;; APPLICANT: Zamudio, Carlos  
;; APPLICANT: Eroshkin, Alexey M  
;; APPLICANT: Lemieux, Sebastien M  
;; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
;; FILE REFERENCE: 10182-018-999  
;; CURRENT APPLICATION NUMBER: US/10/128,714  
;; CURRENT FILING DATE: 2002-04-23  
;; PRIOR APPLICATION NUMBER: US 60/285,697  
;; PRIOR FILING DATE: 2001-04-23  
;; PRIOR APPLICATION NUMBER: US 60/287,066  
;; PRIOR FILING DATE: 2001-04-27  
;; PRIOR APPLICATION NUMBER: US 60/295,890  
;; PRIOR FILING DATE: 2001-06-05  
;; PRIOR APPLICATION NUMBER: US 60/303,899  
;; PRIOR FILING DATE: 2001-07-09  
;; PRIOR APPLICATION NUMBER: US 60/316,362  
;; PRIOR FILING DATE: 2001-08-31  
;; NUMBER OF SEQ ID NOS: 8603  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 8288  
;; LENGTH: 1199  
;; TYPE: PRT  
;; ORGANISM: Aspergillus fumigatus  
US-10-128-714-8288

Query Match 61.8%; Score 34; DB 15; Length 1199;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

2 VSLTAYAMD 10  
:|||||  
212 MSLTSYSMD 220

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RESULT 10
US-09-741-669-402
; Sequence 402, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forevch, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT FILING DATE: US/09/741,669
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; SOFTWARE: FaalSeq for Windows Version 4.0
; SEQ ID NO 402
; LENGTH: 1653
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-402

Query Match          61.8%; Score 34; DB 9; Length 1653;
Best Local Similarity 75.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 LTRAYAMDY 11
Db      1253 LTRAYMDF 1260

RESULT 11
US-09-880-748-2309
; Sequence 2309, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2309
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2309

Query Match          60.0%; Score 33; DB 11; Length 16;
Best Local Similarity 55.6%; Pred. No. 5.3;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3 LTRAYAMDY 11
Db      5 LTRAYMDF 13

RESULT 12
US-09-925-299-999
; Sequence 999, Application US/09925299
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; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 999
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-999

Query Match          60.0%; Score 33; DB 9; Length 130;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 VSLTRAYAMDY 11
Db      88 MKLTRAYMDF 97

RESULT 13
US-09-925-299-999
; Sequence 999, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 999
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-999

Query Match          60.0%; Score 33; DB 11; Length 130;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 VSLTRAYAMDY 11
Db      88 MKLTRAYMDF 97

RESULT 14
US-09-880-748-231
; Sequence 231, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 231  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-231

Query Match 60.0%; Score 33; DB 11; Length 251;  
 Best Local Similarity 55.6%; Pred. No. 1e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

3 SLTAYAMDY 11  
 :||:|:|  
 103 TLTSYVLDY 111

RESULT 15  
 US-10-238-075-368  
 ; Sequence 368, Application US/10238075  
 ; Publication No. US20030148324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: I.N.S.E.R.M.  
 ; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat  
 ; FILE REFERENCE: BLANDINE  
 ; CURRENT APPLICATION NUMBER: US/10/238,075  
 ; PRIOR FILING DATE: 2002-09-10  
 ; PRIOR APPLICATION NUMBER: 0003145  
 ; PRIOR FILING DATE: 2000-03-10  
 ; NUMBER OF SEQ ID NOS: 1576  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 368  
 ; LENGTH: 329  
 ; TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 US-10-238-075-368

Query Match 60.0%; Score 33; DB 12; Length 329;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 2 VSLTAYAMDY 11  
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 64 IAITAYGMTY 73

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 Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:39:02 ; Search time 15.95 Seconds  
(without alignments)  
29.180 Million cell updates/sec

Title: US-09-759-112a-19  
Perfect score: 55  
Sequence: 1 RVSLTAYAMDY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
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Listing first 45 summaries

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3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
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6: /cgn2\_6/prodata/1/1aa/backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	39	3	US-08-984-277-10
2	42	76.4	120	2	US-08-652-558-4
3	42	76.4	120	2	US-08-652-558-5
4	42	76.4	120	2	US-08-652-558-6
5	42	76.4	120	2	US-08-652-558-7
6	42	76.4	120	2	US-08-652-558-8
7	42	76.4	120	2	US-08-652-558-9
8	42	76.4	120	2	US-08-652-558-38
9	42	76.4	120	3	US-09-254-189-2
10	42	76.4	120	3	US-09-254-189-3
11	42	76.4	120	3	US-09-254-189-4
12	42	76.4	120	3	US-09-254-189-5
13	42	76.4	120	3	US-09-254-189-6
14	34	61.8	130	4	US-08-466-151-5
15	34	61.8	130	4	US-08-466-151-6
16	34	61.8	138	3	US-08-513-968-4
17	34	61.8	138	3	US-09-070-637-20
18	34	61.8	738	1	US-07-985-458-3
19	33	60.0	452	1	US-08-275-488A-2
20	33	60.0	452	1	US-08-275-490-2
21	33	60.0	452	1	US-08-446-380-2
22	33	60.0	452	1	US-08-446-374-2
23	33	60.0	452	1	US-08-445-801-2
24	33	60.0	452	1	US-08-445-801-2
25	33	60.0	452	1	US-08-487-2
26	33	60.0	452	5	PCT-US95-08919-2
27	33	60.0	453	1	US-08-275-488A-12

28	33	60.0	453	1	US-08-275-490-12	Sequence 12, Appl
29	33	60.0	453	1	US-08-446-380-12	Sequence 12, Appl
30	33	60.0	453	1	US-08-446-374-12	Sequence 12, Appl
31	33	60.0	453	1	US-08-446-382-12	Sequence 12, Appl
32	33	60.0	453	1	US-08-445-801-12	Sequence 12, Appl
33	33	60.0	453	1	US-08-275-487-12	Sequence 12, Appl
34	33	60.0	453	5	PCT-US95-08919-12	Sequence 12, Appl
35	33	60.0	494	1	US-08-275-488A-4	Sequence 4, Appl
36	33	60.0	494	1	US-08-275-490-4	Sequence 4, Appl
37	33	60.0	494	1	US-08-446-380-4	Sequence 4, Appl
38	33	60.0	494	1	US-08-446-374-4	Sequence 4, Appl
39	33	60.0	494	1	US-08-446-382-4	Sequence 4, Appl
40	33	60.0	494	1	US-08-445-801-4	Sequence 4, Appl
41	33	60.0	494	1	US-08-275-487-4	Sequence 4, Appl
42	33	60.0	494	5	PCT-US95-08919-4	Sequence 4, Appl
43	33	60.0	601	4	US-09-252-991A-30589	Sequence 30589, A
44	32	58.2	130	4	US-09-252-991A-23553	Sequence 23553, A
45	32	58.2	147	2	US-08-579-940-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-984-277-10  
; Sequence 10, Application US/08984277  
; Patent No. 6057421  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/984,277  
; FILING DATE: 3-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca, Daniel  
; REGISTRATION NUMBER: 42,368  
; REFERENCE/DOCKET NUMBER: 50200-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-756-8600  
; TELEFAX: 202-756-8699  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-984-277-10  
Query Match 100.0%; Score 55; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. NO. 0.00015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RVSLTAYAMDY 11

Db 18 RVSLTAVAMDY 28

## RESULT 2

US-08-652-558-4  
Sequence 4, Application US/08652558

Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-558-4

ry Match 76.4%; Score 42; DB 2; Length 120;

c Local Similarity 72.7%; Pred. No. 0.25;

ches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAVAMDY 11

Db 99 RVATATLYAMDY 109

## RESULT 3

US-08-652-558-5

Sequence 5, Application US/08652558

Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-558-5

Query Match 76.4%; Score 42; DB 2; Length 120;

Best Local Similarity 72.7%; Pred. No. 0.25;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAVAMDY 11

Db 99 RVATATLYAMDY 109

## RESULT 4

US-08-652-558-6

Sequence 6, Application US/08652558

Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-558-6

Query Match 76.4%; Score 42; DB 2; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSATVAMDY 11  
||:|||||  
Db 99 RVTATLYAMDY 109

RESULT 5  
US-08-652-558-7  
Sequence 7, Application US/08652558  
Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES  
THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-558-7

Query Match 76.4%; Score 42; DB 2; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSATVAMDY 11  
||:|||||  
Db 99 RVTATLYAMDY 109

RESULT 6  
US-08-652-558-8  
Sequence 8, Application US/08652558  
Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER & WITCOFF  
STREET: 75 STATE STREET, 23RD FLOOR  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9111

TELEFAX: 617-345-9100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-558-8

Query Match 76.4%; Score 42; DB 2; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSATVAMDY 11  
||:|||||  
Db 99 RVTATLYAMDY 109

RESULT 7  
US-08-652-558-9  
Sequence 9, Application US/08652558  
Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.  
REGISTRATION NUMBER: 30,237  
REFERENCE/DOCKET NUMBER: 95,497-L  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-558-9

Query Match 76.4%; Score 42; DB 2; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 RVSLEYAMDY 11  
||: |||||  
99 RVTATLYAMDY 109

RESULT 8  
US-08-652-558-38  
Sequence 38, Application US/08652558  
Patent No. 5861155  
GENERAL INFORMATION:  
APPLICANT: LIN, AUGUSTINE YEE-THARN  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER & WITCORP  
STREET: 75 STATE STREET, 23RD FLOOR  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,558  
FILING DATE: JUNE 6, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB94/00387  
FILING DATE: NOVEMBER 21, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: YANKWICH, LEON R.  
REGISTRATION NUMBER: 30,237  
REFERENCE/DOCKET NUMBER: 95,497-L  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-558-38

Query Match 76.4%; Score 42; DB 2; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
1 RVSLEYAMDY 11  
||: |||||

Db 99 RVTATLYAMDY 109

RESULT 9  
US-09-254-189-2  
Sequence 2, Application US/09254189  
Patent No. 6150792  
GENERAL INFORMATION:  
APPLICANT: Lundquist, Tomas  
TITLE OF INVENTION: Sequence Listing  
FILE REFERENCE: 3526/00000  
CURRENT APPLICATION NUMBER: US/09/254,189  
CURRENT FILING DATE: 1999-03-02  
EARLIER APPLICATION NUMBER: 00/000,000  
EARLIER FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-254-189-2

Query Match 76.4%; Score 42; DB 3; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLEYAMDY 11  
||: |||||  
Db 99 RVTATLYAMDY 109

RESULT 10  
US-09-254-189-3  
Sequence 3, Application US/09254189  
Patent No. 6150792  
GENERAL INFORMATION:  
APPLICANT: Lundquist, Tomas  
TITLE OF INVENTION: Sequence Listing  
FILE REFERENCE: 3526/00000  
CURRENT APPLICATION NUMBER: US/09/254,189  
CURRENT FILING DATE: 1999-03-02  
EARLIER APPLICATION NUMBER: 00/000,000  
EARLIER FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-254-189-3

Query Match 76.4%; Score 42; DB 3; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLEYAMDY 11  
||: |||||  
Db 99 RVTATLYAMDY 109

RESULT 11  
US-09-254-189-4  
Sequence 4, Application US/09254189  
Patent No. 6150792

```

; GENERAL INFORMATION:
; APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
; Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
; EARLIER APPLICATION NUMBER: 00/000,000
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; OTHER INFORMATION: monoclonal antibody
; US-254-189-4

Query Match          76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVSATVAMDY 11
Db 99 RVTATLVAMDY 109

RESULT 12
US-09-254-189-5
; Sequence 5, Application US/09254189
; Patent No. 6150792
; GENERAL INFORMATION:
; APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
; Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
; EARLIER APPLICATION NUMBER: 00/000,000
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; OTHER INFORMATION: monoclonal antibody
; US-09-254-189-5

Query Match          76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVSATVAMDY 11
Db 99 RVTATLVAMDY 109

RESULT 13
US-09-254-189-6
; Sequence 6, Application US/09254189
; Patent No. 6150792
; GENERAL INFORMATION:
; APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
; Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
```

```

; EARLIER APPLICATION NUMBER: 00/000,000
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; OTHER INFORMATION: monoclonal antibody
; US-09-254-189-6

Query Match          76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVSATVAMDY 11
Db 99 RVTATLVAMDY 109

RESULT 14
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P071BP2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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US-08-466-151-5

Query Match 61.8%; Score 34; DB 3; Length 130;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 LTRAYAMDY 11  
: |||||  
Db 99 VVAYAMDY 106

RESULT 15  
US-08-466-163B-5  
; Sequence 5, Application US/08466163B  
; Patent No. 6329509

; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2CID1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
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; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 5  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-466-163B-5

Query Match 61.8%; Score 34; DB 4; Length 130;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 LTRAYAMDY 11  
: |||||  
Db 99 VVAYAMDY 106

Search completed: September 10, 2003, 17:43:22  
Web time : 15.95 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:34:16 ; Search time 39.05 Seconds  
(without alignments)  
44.712 Million cell updates/sec

Title: US-09-759-112A-19  
Perfect score: 55  
Sequence: 1 RVSLTAYAMDY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                  Listing first 45 summaries
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22:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

## SUMMARIES

Result *	No.	Score	Query Match	Length	DB	ID	Description
	1	55	100.0	11	23	AAO18634	Murine Mab 1F7 hea
	2	55	100.0	39	21	AA91019	1F7 antibody varia
	3	55	100.0	121	23	AAO18528	Murine Mab 1F7 hea
	4	42	76.4	120	20	AA922433	TM27 antibody VH c
	5	42	76.4	120	20	AA922429	TM27 antibody VH c
	6	42	76.4	120	20	AA922430	TM27 antibody VH c
	7	42	76.4	120	20	AA922431	TM27 antibody VH c
	8	42	76.4	120	20	AA922432	TM27 antibody VH c
	9	37	67.3	378	22	ABG09046	Novel human diagno

10	37	67.3	391	23	ABP43855
11	37	67.3	1212	24	AAO164333
12	35	63.6	120	16	AAK733030
13	35	63.6	424	21	AAI91067
14	34	61.8	119	10	AAIP905404
15	34	61.8	119	13	AAK245555
16	34	61.8	119	13	AAK245555
17	34	61.8	119	13	AAK245555
18	34	61.8	119	13	AAK245555
19	34	61.8	119	13	AAK245555
20	34	61.8	119	13	AAK245555
21	34	61.8	119	13	AAK245555
22	34	61.8	130	14	AAK333080
23	34	61.8	130	21	AAK811968
24	34	61.8	138	10	AAIP905443
25	34	61.8	143	21	AAI43864
26	34	61.8	249	21	AAI69522
27	34	61.8	370	22	AAK943666
28	34	61.8	370	23	AAE217111
29	34	61.8	370	24	AAO1637575
30	34	61.8	370	24	AAO1637575
31	34	61.8	633	12	AAK877666
32	34	61.8	738	12	AAK139999
33	34	61.8	738	13	AAK139999
34	34	61.8	742	11	AAK052355
35	34	61.8	1446	24	ABJ25630
36	34	61.8	1199	24	ABJ262330
37	34	61.8	1653	22	AAK983545
38	33.5	60.9	247	9	AAK80155
39	33.5	60.9	247	9	AAK80156
40	33.5	60.9	466	5	AAAP0032
41	33	60.0	16	23	AAK462898
42	33	60.0	61	21	AAAG212333
43	33	60.0	80	21	AAAG212333
44	33	60.0	91	21	AAAG54799
45	33	60.0	106	21	AAAG212333

## ALIGNMENTS

RESULT 1	
AA018534	
ID	AA018534 standard; Peptide: 11 AA.
XX	
AC	AA018534;
XX	
DT	11-OCT-2002 (first entry)
XX	
DE	Murine Mab 1F7 heavy chain CDR3 region.
XX	
KW	Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR:
KM	complementarity determining region; framework-determining region;
KX	FR; heavy chain; light chain; HIV infection.
XX	
OS	Mus sp.
XX	
PN	WO200255668-A2.
XX	
PD	18-JUL-2002.
XX	
PF	11-JAN-2002; 2002WO-US00927.
XX	
FR	11-JAN-2001; 2001US-0759112.
XX	
PA	(IMMP-) IMMPHERON INC.
XX	
PI	Muller S, Kohler H;
XX	
DR	WPI; 2002-590668/63.
DR	N-PSDB; AAL48658.
XX	
PT	New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate  
PT anti-human immunodeficiency virus (HIV) antibodies, for use in  
PT vaccines against HIV -

PS Claim 4, Page 22, 27pp; English.

CC The present invention relates to coding sequences of the murine 1F7  
CC anti-idiotypic antibody complementarity-determining region (CDR) or  
CC framework-determining region (FR). The antibody binds to human or primate  
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
CC treatment of HIV infection. The present sequence is a region of the 1F7  
CC heavy chain.

XX Sequence 11 AA;

Query Match 100.0%; Score 55; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;

1 RVSLLTAYAMDY 11  
|||||  
1 RVSLLTAYAMDY 11

RESULT 2

AAV91019 standard; protein; 39 AA.

AAV91019;

05-SEP-2000 (first entry)

1F7 antibody variable heavy chain H3 amino acid sequence SEQ ID NO:10.

1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;  
AIDS; anti-HIV; human immunodeficiency virus; detection;

acquired immunodeficiency syndrome.

Mus sp.

US6057421-A.

02-MAY-2000.

03-DEC-1997; 97US-0984277.

30-NOV-1994; 94US-0351193.

(IMMP-) IMPHERON INC.

Muller S, Kohler H;

WPI; 2000-338622/29.

Variable heavy and light chain regions of murine monoclonal antibody  
1F7, useful for treating HIV infection and AIDS -

Claim 1, Fig 8; 45pp; English.

XX The present invention describes the variable heavy and light chain  
CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAV91014 to  
CC AAV91016 represent specifically claimed amino acid sequences of the  
CC variable light chain, and AAV91017 to AAV91019 represent specifically  
CC claimed amino acid sequence of the variable heavy chain. The antibodies  
CC are used for treatment of HIV (human immunodeficiency virus) infection  
CC and AIDS (acquired immunodeficiency syndrome). They are also used for  
CC detecting HIV in serum and for stimulating HIV antigen related and  
CC committed B cells to produce broadly reactive and neutralising antibodies  
CC by clonotypic stimulation.

Sequence 39 AA;

Query; Match 100.0%; Score 55; DB 21; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.00049;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVSLLTAYAMDY 11  
|||||  
Db 18 RVSLLTAYAMDY 28

RESULT 3

AA018528 standard; Protein; 121 AA.

AA018528;

11-OCT-2002 (first entry)

Murine Mab 1F7 heavy chain.

Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
KW complementarity determining region; framework-determining region;  
KW FR; heavy chain; light chain; HIV infection.

Mus sp.

WO200255668-A2.

18-JUL-2002.

11-JAN-2002; 2002WO-US00927.

11-JAN-2001; 2001US-0759112.

(IMMP-) IMPHERON INC.

Muller S, Kohler H;

WPI; 2002-590668/63.

N-PSDB; AAL48652.

New polynucleotide encoding a complementarity- or framework-determining  
PT region of an anti-idiotypic antibody that binds to human or primate  
PT anti-human immunodeficiency virus (HIV) antibodies, for use in  
PT vaccines against HIV -

Disclosure; Page 18-19; 27pp; English.

The present invention relates to coding sequences of the murine 1F7  
CC anti-idiotypic antibody complementarity-determining region (CDR) or  
CC framework-determining region (FR). The antibody binds to human or primate  
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
CC treatment of HIV infection. The present sequence is the 1F7 heavy chain.

Sequence 121 AA;

Query Match 100.0%; Score 55; DB 23; Length 121;

Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVSLLTAYAMDY 11  
|||||  
Db 100 RVSLLTAYAMDY 110

RESULT 4

AA122433 standard; protein; 120 AA.

AA122433;

28-SEP-1999 (first entry)

TM27 antibody VH chain mutant V92R.

Sequence 120 AA;

Query; Match 100.0%; Score 55; DB 21; Length 120;

Query; Match 100.0%; Score 55; DB 21; Length 39;

Query; Match 100.0%; Score 55; DB 21; Length 39;

Query; Match 100.0%; Score 55; DB 21; Length 39;

KW Igg antibody; TM27; variable chain; immunoglobulin G; medical therapy;  
KM autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;  
heavy chain.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 92  
FT /label= V92R  
XX  
PN WO9937329-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 15-JAN-1999; 99WO-SE00049.  
XX  
PR 09-MAR-1998; 98SE-0000766.  
PR 22-JAN-1998; 98SE-0000170.  
XX  
XX (ASTR ) ASTRA AB.  
XX  
XX Flink O, Petren S;  
XX  
DR WPI: 1999-458611/38.  
XX  
PT Isotonic pharmaceutical antibody formulations comprising a citrate  
buffer, have improved storage  
XX  
PS Claim 12; Page 25-26; 30pp; English.  
XX  
XX This sequence is a mutant of the variable heavy (VH) chain of the  
antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in  
the isotonic pharmaceutical formulation of the invention, along with a  
citrate buffer at a physiologically acceptable pH. The formulations are  
useful in medical therapy, especially for treatment of autoimmune  
disease, and particularly, therapy of multiple sclerosis (using the TM27  
antibody heavy or light chains). The formulation is useful for improving  
the storage of an antibody. The antibody formulations are simple and  
effective. The formulations are stable and have improved storage  
properties. The formulation is simpler than prior art formulations.  
Existing antibody formulations require the use both of a stabiliser and a  
buffer. The present invention formulations are stabilized only by citrate  
buffer in a saline solution at a physiologically preferable pH. The  
avoidance of low pH prevents undesirable reaction as the site of  
injection. The formulation does not use ovalbumin for stabilisation,  
hence avoiding an allergic response to ovalbumin. Also the formulation  
does not require lyophilisation which is an expensive process and also  
requires the formulation to be resuspended prior to administration.

Sequence 120 AA;  
Query Match 76.4%; Score 42; DB 20; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.8;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTPAYAMDY 11  
||:|||||  
Db 99 RVTATLYAMDY 109

RESULT 5  
AAV22429 standard; protein; 120 AA.  
XX  
AC AAV22429;  
XX  
DT 28-SEP-1999 (first entry)  
XX  
DE TM27 antibody VH chain.  
XX  
KM Igg antibody; TM27; variable chain; immunoglobulin G; medical therapy;  
KM autoimmune disease; multiple sclerosis; antibody storage; VH;  
heavy chain.

XX  
OS Homo sapiens.  
XX  
PN WO9937329-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 15-JAN-1999; 99WO-SE00049.  
XX  
PR 09-MAR-1998; 98SE-0000766.  
PR 22-JAN-1998; 98SE-0000170.  
XX  
XX (ASTR ) ASTRA AB.  
XX  
XX Flink O, Petren S;  
XX  
DR WPI: 1999-458611/38.  
XX  
PT Isotonic pharmaceutical antibody formulations comprising a citrate  
buffer, have improved storage  
XX  
PS Claim 12; Page 11; 30pp; English.  
XX  
XX This sequence represents the variable heavy (VH) chain of the  
antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in  
the isotonic pharmaceutical formulation of the invention, along with a  
citrate buffer at a physiologically acceptable pH. The formulations are  
useful in medical therapy, especially for treatment of autoimmune  
disease, and particularly, therapy of multiple sclerosis (using the TM27  
antibody heavy or light chains). The formulation is useful for improving  
the storage of an antibody. The antibody formulations are simple and  
effective. The formulations are stable and have improved storage  
properties. The formulation is simpler than prior art formulations.  
Existing antibody formulations require the use both of a stabiliser and a  
buffer. The present invention formulations are stabilized only by citrate  
buffer in a saline solution at a physiologically preferable pH. The  
avoidance of low pH prevents undesirable reaction as the site of  
injection. The formulation does not use ovalbumin for stabilisation,  
hence avoiding an allergic response to ovalbumin. Also the formulation  
does not require lyophilisation which is an expensive process and also  
requires the formulation to be resuspended prior to administration.

Sequence 120 AA;  
Query Match 76.4%; Score 42; DB 20; Length 120;  
Best Local Similarity 72.7%; Pred. No. 0.8;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTPAYAMDY 11  
||:|||||  
Db 99 RVTATLYAMDY 109

RESULT 6  
AAV22430 standard; protein; 120 AA.  
XX  
AC AAV22430;  
XX  
DT 28-SEP-1999 (first entry)  
XX  
DE TM27 antibody VH chain mutant L461.  
XX  
KM Igg antibody; TM27; variable chain; immunoglobulin G; medical therapy;  
KM autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;  
heavy chain.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 48  
FT /label= L461  
XX

PN MO9937329-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 15-JAN-1999; 99WO-SE00049.  
 XX  
 PR 09-MAR-1998; 98SE-0000766.  
 XX  
 PR 22-JAN-1998; 98SE-0000170.  
 XX  
 PA (ASTR ) ASTRA AB.  
 XX  
 PI Flink O, Petren S;  
 XX  
 PI WPI; 1999-458611/38.  
 DR  
 XX  
 PT Isotonic pharmaceutical antibody formulations comprising a citrate  
 PT buffer, have improved storage  
 XX  
 PS Claim 12; Page 20-21; 30pp; English.  
 CC This sequence is a mutant of the variable heavy (VH) chain of the  
 CC antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in  
 CC the isotonic pharmaceutical formulation of the invention, along with a  
 CC citrate buffer at a physiologically acceptable pH. The formulations are  
 CC useful in medical therapy, especially for treatment of autoimmune  
 CC disease, and particularly, therapy of multiple sclerosis (using the TM27  
 CC antibody heavy or light chains). The formulation is useful for improving  
 CC the storage of an antibody. The antibody formulations are simple and  
 CC effective. The formulations are stable and have improved storage  
 CC properties. The formulations are simpler than prior art formulations.  
 CC Existing antibody formulations require the use both of a stabiliser and a  
 CC buffer. The present invention formulations are stabilized only by citrate  
 CC buffer in a saline solution at a physiologically preferable pH. The  
 CC avoidance of low pH prevents undesirable reaction at the site of  
 CC injection. The formulation does not use ovalbumin for stabilisation,  
 CC hence avoiding an allergic response to ovalbumin. Also the formulation  
 CC does not require lyophilisation which is an expensive process and also  
 CC requires the formulation to be resuspended prior to administration.  
 CC  
 SO Sequence 120 AA;  
 Query Match 76.4%; Score 42; DB 20; Length 120;  
 Best Local Similarity 72.7%; Pred. No. 0.8;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RVSLTAYAMDY 11  
 ||: |||||  
 99 RVTATLYAMDY 109  
 RESULT 7  
 ID AAY22431 standard; protein; 120 AA.  
 AC AAY22431;  
 XX  
 DT 28-SEP-1999 (first entry)  
 XX  
 DE TM27 antibody VH chain mutant F78V, S79F.  
 XX  
 KW IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;  
 KW autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;  
 KW heavy chain.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 78 /label= F78V  
 FT Misc-difference 79 /label= S79F  
 FT  
 FT  
 PN MO9937329-A1.

XX  
 PD 29-JUL-1999.  
 XX  
 PF 15-JAN-1999; 99WO-SE00049.  
 XX  
 PR 09-MAR-1998; 98SE-0000766.  
 XX  
 PR 22-JAN-1998; 98SE-0000170.  
 XX  
 PA (ASTR ) ASTRA AB.  
 XX  
 PI Flink O, Petren S;  
 XX  
 PI WPI; 1999-458611/38.  
 DR  
 XX  
 PT Isotonic pharmaceutical antibody formulations comprising a citrate  
 PT buffer, have improved storage  
 XX  
 PS Claim 12; Page 22-23; 30pp; English.  
 CC This sequence is a mutant of the variable heavy (VH) chain of the  
 CC antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in  
 CC the isotonic pharmaceutical formulation of the invention, along with a  
 CC citrate buffer at a physiologically acceptable pH. The formulations are  
 CC useful in medical therapy, especially for treatment of autoimmune  
 CC disease, and particularly, therapy of multiple sclerosis (using the TM27  
 CC antibody heavy or light chains). The formulation is useful for improving  
 CC the storage of an antibody. The antibody formulations are simple and  
 CC effective. The formulations are stable and have improved storage  
 CC properties. The formulations are simpler than prior art formulations.  
 CC Existing antibody formulations require the use both of a stabiliser and a  
 CC buffer. The present invention formulations are stabilized only by citrate  
 CC buffer in a saline solution at a physiologically preferable pH. The  
 CC avoidance of low pH prevents undesirable reaction at the site of  
 CC injection. The formulation does not use ovalbumin for stabilisation,  
 CC hence avoiding an allergic response to ovalbumin. Also the formulation  
 CC does not require lyophilisation which is an expensive process and also  
 CC requires the formulation to be resuspended prior to administration.  
 CC  
 SO Sequence 120 AA;  
 Query Match 76.4%; Score 42; DB 20; Length 120;  
 Best Local Similarity 72.7%; Pred. No. 0.8;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RVSLTAYAMDY 11  
 ||: |||||  
 99 RVTATLYAMDY 109  
 RESULT 8  
 ID AAY22432 standard; protein; 120 AA.  
 AC AAY22432;  
 XX  
 DT 28-SEP-1999 (first entry)  
 XX  
 DE TM27 antibody VH chain mutant V67L, T68S, M69I, L70S, T73N.  
 XX  
 KW IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;  
 KW autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;  
 KW heavy chain.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 67 /label= V67L  
 FT Misc-difference 68 /label= T68S  
 FT Misc-difference 69 /label= T68S  
 FT Misc-difference 70 /label= M69I  
 FT



FT Misc-difference /label= L70S  
 FT 73 /label= T73N  
 XX  
 XX  
 PN WO9937329-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PD 15-JAN-1999; 99WO-SE00049.  
 XX  
 PR 09-MAR-1998; 98SE-0000766.  
 PR 22-JAN-1998; 98SE-0000170.  
 XX  
 PA (ASTR ) ASTRA AB.  
 XX  
 PI Flink O, Petren S;  
 XX  
 DR WPI, 1999-458611/38.

Isotonic pharmaceutical antibody formulations comprising a citrate buffer, have improved storage

Claim 12; Page 23-24; 30pp; English.

CC This sequence is a mutant of the variable heavy (VH) chain of the  
 CC antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in  
 CC the isotonic pharmaceutical formulation of the invention, along with a  
 CC citrate buffer at a physiologically acceptable pH. The formulations are  
 CC useful in medical therapy, especially for treatment of autoimmune  
 CC disease, and particularly, therapy of multiple sclerosis (using the TM27  
 CC antibody heavy or light chains). The formulation is useful for improving  
 CC the storage of an antibody. The antibody formulations are simple and  
 CC effective. The formulations are stable and have improved storage  
 CC properties. The formulation is simpler than prior art formulations.  
 CC Existing antibody formulations require the use both of a stabiliser and a  
 CC buffer. The present invention formulations are stabilized only by citrate  
 CC buffer in a saline solution at a physiologically preferable pH. The  
 CC avoidance of low pH prevents undesirable reaction as the site of  
 CC infection. The formulation does not use ovalbumin for stabilisation,  
 CC hence avoiding an allergic response to ovalbumin. Also the formulation  
 CC does not require lyophilisation which is an expensive process and also  
 CC requires the formulation to be resuspended prior to administration.

SQ Sequence 120 AA;

Query Match 76.4%; Score 42; DB 20; Length 120;  
 Beet Local Similarity 72.7%; Pred. No. 0.8;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 RVSITAVAMDY 11  
 ||:|||||  
 99 RVTATLIVAMDY 109

RESULT 9  
 ABG09046

ID ABG09046 standard; Protein; 378 AA.

AC ABG09046;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #9037.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW Food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI, 2001-639362/73.  
 DR N-PSDB; AAS73233.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

Claim 20; SEQ ID No 39405; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 378 AA;

Query Match 67.3%; Score 37; DB 22; Length 378;  
 Beet Local Similarity 54.5%; Pred. No. 31;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 RVSITAVAMDY 11  
 ||:|||||  
 300 KMSLNAVVALDF 310

RESULT 10  
 ABP43853

ID ABP43853 standard; Protein; 391 AA.

AC ABP43853;

DT 26-FEB-2003 (first entry)

DE FLJ20035 fls clone.

XX Neuroprotective; immunomodulator; cancer; chromosome 12;

KW cytostatic; anti-inflammatory; gene therapy; nutritional supplement;

KW wound; ulcer; Alzheimer's disease; Huntington's disease;

KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;

XX vulnerability.

OS Homo sapiens.

XX WO200231111-A2.

PD 18-APR-2002.

XX 11-OCT-2001; 2001MO-US27760.  
XX 12-OCT-2000; 2000US-0687527.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Auendi V, Zhang J, Zhao QA, Ren F,  
XX Xue AJ, Yang Y, Wehrman T, Dzmanac RT;  
XX WPI; 2002-426278/45.  
XX N-PSDB; ABO61097.  
XX New polypeptides and their encoded proteins, useful as nutritional  
XX sources or supplements, or in gene therapy, particularly for treating  
XX wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
XX inflammation -  
XX Claim 20; SEQ ID # 756; 357pp + sequence listing; English.

The invention relates to 446 newly isolated polynucleotide sequences.  
The activity of polynucleotides of the invention may be described as,  
vulnerable, neuroprotective, immunomodulator, cytostatic and  
anti-inflammatory. Compositions comprising nucleic acids of the invention  
are useful for treating a mammalian subject, or as nutritional sources or  
supplements. These are useful in gene therapy, particularly for treating  
wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
CC inflammation. The nucleic acids and polypeptides are also useful in  
CC diagnostic and research methods. The sequences given in records  
CC APP43544-AB843989 represent polypeptides encoded by polynucleotides of  
CC the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ffp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 391 AA;

Query Match 67.3%; Score 37; DB 23; Length 391;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLLTAYAMDY 11  
DB 314 KMSLNAYALDF 324

RESULT 11

6433  
AAO16433 standard; Protein; 1712 AA.

AC AAO16433;

XX 10-APR-2003 (first entry)

DE Human nucleic acid-associated protein (NAAP) - SEQ ID NO 30.

XX Human, nucleic acid-associated protein; NAAP; aretiolosciosis;  
XX cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS;  
XX cancer; developmental disorder; renal tubular acidosis; anemia; asthma;  
XX mental retardation; neurological disorder; Alzheimer's disease; epilepsy;  
XX Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;  
XX Crohn's disease; transgenic animal; animal model.

XX Homo sapiens.

XX OS

XX PN MO2003000864-A2.

XX 03-JAN-2003.

XX 20-JUN-2002; 2002MO-US21179.  
XX 22-JUN-2001; 2001US-300518P.

PR 29-JUN-2001; 2001US-301787P.  
PR 29-JUN-2001; 2001US-301792P.  
PR 29-JUN-2001; 2001US-301892P.  
PR 29-JUN-2001; 2001US-301893P.  
PR 06-JUL-2001; 2001US-303405P.  
PR 06-JUL-2001; 2001US-303442P.  
PR 15-MAR-2002; 2002US-364438P.

XX (INCY-) INCYTE GENOMICS INC.

XX Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM;  
XX Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe ID;  
XX Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR;  
XX Borowsky M, Yao MG, Walla NK, Bandman O, Lai PG, Becha SD;  
XX Lee SY, Richardson TW, Elliott VS, Luo W, Tang YT, Zeharjadian Y;  
XX Lu Y;  
XX WPI; 2003-201420/19.  
XX N-PSDB; AAL51583.

XX New nucleic acid-associated proteins and polynucleotides, useful for  
XX diagnosing, treating or preventing cell proliferative (e.g. cancer),  
XX neurological (e.g. epilepsy or Parkinson's disease), or autoimmune  
XX disorders (e.g. AIDS) -  
XX Claim 1; Page 262-266; 312pp; English.

XX The invention comprises the amino acid and coding sequences of human  
XX nucleic acid-associated proteins (NAAP). The DNA and protein sequences of  
XX the invention are useful for diagnosing, treating or preventing disorders  
XX associated with aberrant expression of NAAP, such as: cell proliferative  
XX disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis  
XX or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia  
XX or mental retardation); neurological disorders (e.g. Alzheimer's disease,  
XX Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders  
XX (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of  
XX the invention are useful for creating transgenic animals to model human  
XX disease. The present amino acid sequence represents a human nucleic acid-  
XX associated protein of the invention.

XX Sequence 1712 AA;

Query Match 67.3%; Score 37; DB 24; Length 1712;  
Best Local Similarity 54.5%; Pred. No. 1,7e+02;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLLTAYAMDY 11  
DB 1635 KMSLNAYALDF 1645

RESULT 12

AA77303  
ID AAR77303 standard; peptide; 120 AA.

AC AAR77303;

XX 25-MAR-2003 (updated)

DT 23-NOV-1995 (first entry)

XX Variable heavy chain sequence of humanised antibody chain TM27 VH.  
XX Humanised antibody; TM27; T cell; multiple sclerosis.

XX Synthetic.

XX OS

XX FH Key

XX Region 31..35

XX Region 50..64  
XX Region 98..109  
XX Region 1/label= CDR1  
XX Region 1/label= CDR2  
XX Region 1/label= CDR3

XX WO9516038-A2.  
 XX 15-JUN-1995.  
 PD  
 XX 21-NOV-1994; 94WO-IB00387.  
 XX  
 XX 08-DEC-1993; 93GB-0025182.  
 PR  
 XX (MERC/) MERCER C P.  
 PA (TCEL-) T CELL SCT INC.  
 XX Lin AY;  
 PI  
 XX WPI; 1995-224322/29.  
 DR  
 XX Humanised antibody specific for select sub-population of T cells  
 PT useful for treatment of Crohn's disease and Multiple Sclerosis

Claim 3; Page 81; 92pp; English.

CC A mouse monoclonal antibody (mAb), TM23, which recognises human V  
 CC beta 5.2 and 5.3, was humanised by CDR grafting into NEMM heavy  
 CC chain and REI light chain frameworks. The cDNAs encoding humanised  
 CC heavy (IgG1) and light (K) chains in mammalian cell expression  
 CC vectors with Neo and DHFR selection markers, respectively, were  
 CC transfected into a DHFR- Chinese hamster fibroblast (CHO) cell line  
 CC followed by selection and amplification. The humanised mAb that was  
 CC secreted was designated "TM27", and maintains specificity for human  
 CC TCR V beta 5.2 and 5.2. It is used as a therapeutic agent for human  
 CC multiple sclerosis. TM27 is a mutant with Leu at posn. 48 of heavy  
 CC chain.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 120 AA;

Query Match 63.6%; Score 35; DB 16; Length 120;  
 Best Local Similarity 70.0%; Pred. No. 22;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLLRAYAMD 10  
 ||:|||||  
 Db 99 RVTATLYAMD 108

RESULT 13

AA91067  
 AA91067 standard; Protein; 424 AA.

AA91067;

08-SEP-2000 (first entry)

Streptomyces nogalater nogalamycin biosynthesis ORF snoge protein.

Streptomyces nogalater; nogalamycin biosynthesis; antibiotic;

anthracycline biosynthetic pathway; gene cluster; drug screening;

antibiotic; antitumour antibiotic; anthracycline.

Streptomyces nogalater.

WO200024775-A1.

04-MAY-2000.

20-OCT-1999; 99WO-FI00870.

23-OCT-1998; 98FI-0002295.

(GALI-) GALILAEUS OY.  
 Ylinen K, Torkkell S, Palmu K, Hakala J;

DR WPI; 2000-350696/30.  
 DR N-PSDB; AAA39283.

PT Isolated and purified DNA fragment for obtaining novel hybrid  
 PT antibiotics comprises the gene cluster for the anthracycline  
 PT biosynthetic pathway of the bacterium Streptomyces nogalater -

Example 1; Page 52-54; 59pp; English.

CC AAA39283 represents the nogalamycin biosynthesis gene cluster isolated  
 CC from Streptomyces nogalater. AA91055 to AA91071 represent ORF protein  
 CC sequences encoded by the gene cluster. Nogalamycin is an anthracycline  
 CC antibiotic, so the nogalamycin biosynthetic pathway is also known as the  
 CC anthracycline biosynthetic pathway. DNA fragments, plasmids and process  
 CC from the present invention are useful for obtaining novel hybrid  
 CC antibiotics, such as anthracyclines (antitumour antibiotics) or  
 CC anthracyclonones.

SQ Sequence 424 AA;

Query Match 63.6%; Score 35; DB 21; Length 424;  
 Best Local Similarity 70.0%; Pred. No. 91;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLLRAYAMD 10  
 ||:|||||  
 Db 2 RVLTLSPAMD 11

RESULT 14

AA90540  
 ID AAP90540 standard; protein; 119 AA.

AA90540;

25-MAR-2003 (updated)

20-OCT-1989 (first entry)

Immunoglobulin H chain variable region.

Immunoglobulin; H chain variable region; HIV.

Mus musculus.

EP327000-A.

09-AUG-1989.

30-JAN-1989; 89EP-0101583.

30-JAN-1988; 88JP-0020255.

08-JUL-1988; 88JP-0171385.

(KAGA) CHERO SERO THERAPEUTIC RES INS.

Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
 Taketsuki K;

WPI; 1989-229050/32.

N-PSDB; AAN90491, AAN90493, AAN90495.

Chimeric anti-human immune virus antibodies - cong. mouse variable  
 PT regions and human constant regions for diagnosis, treatment and  
 PT prevention of AIDS

Claim 2; page 14; 33pp; English.

The H chain variable region is from an immunoglobulin with anti-HIV  
 CC neutralising activity. See AAN90491, AAN90493 and AAN90495.

(Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 119 AA;

Query Match 61.8%; Score 34; DB 10; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 35;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAYAMDY 11  
 :|||||  
 DB 102 SAYAMDY 108

## RESULT 15

AA24555  
 ID AAR24555 standard; Protein; 119 AA.

XX AAR24555;

XX 08-DEC-1992 (first entry)

XX Human x mouse modified anti-HIV antibody Heavy chain.

XX Heavy; light; CDR; HIV; AIDS; FR; framework region.

XX Synthetic.

XX Key Location/Qualifiers

FT 1..29

FT /label= FR1

FT /note= "human antibody derived amino acid sequence"

FT 31..35

FT /label= CDR1

FT 41..47

FT /label= FR2

FT /note= "human antibody derived amino acid sequence"

FT 50..65

FT /label= CDR2

FT 73..97

FT /label= FR3

FT /note= "human antibody derived amino acid sequence"

FT 99..108

FT /label= CDR3

FT 109..119

FT /label= FR4

FT /note= "human antibody derived amino acid sequence"

XX JP04141095-A.

XX 14-MAY-1992.

XX 02-OCT-1990; 90JP-0266091.

XX 02-OCT-1990; 90JP-0266091.

XX (KAGA ) KAGAKU OYOBI KESSEI RYOHO.

XX WPI; 1992-212765/26.

XX New recombinant modified anti-HIV antibodies - comprise human x

XX mouse modified antibody H and L chains

XX Claim 3; Page 1; 15pp; Japanese.

XX The human antibody derived amino acid sequence belongs to the human

XX antibody subgroup I. The CDRs and a part of the amino acid

XX sequence of the neighbouring framework region N- and/or C-terminal

XX are mouse monoclonal antibody derived sequences. The anti-HIV

XX modified antibody can be used for the prophylaxis and treatment of

XX AIDS.

XX Specific examples of the H chain are given in AAR24556-58 and

XX AAR24560-62. A specific example of the L chain is given in AAR24575.

XX Sequence 119 AA;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAYAMDY 11  
 :|||||  
 DB 102 SAYAMDY 108

Search completed: September 10, 2003, 17:40:19  
 Job time : 40.05 secs

Query Match 61.8%; Score 34; DB 13; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 35;